

FIG.1A

```
148      178      208      238      268      298
FRI-1  ALLVFLDII EWTTQETFP PKYLHYDPETGRQLLCKAPGTYLKQHCTVRRKTL CVPCPD
SW: TNR2_HUMAN  HALPAQVAFTPYAPEPGSTCRRLREYYDQTAQMCCSKCSPGQHAKVFCTKTSDTVCDSCED
              30      40      50      60      70      80
328
FRI-1  YSYTDSWHTS
      :||: |:
SW: TNR2_HUMAN  STYTQLWNWVPECLSCGSRSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPL
              90      100     110     120     130     140
```

FIG.1B

```

FRI-1  69 YLHYDPETGRQLLCKAPGTYLKQHC.TVRRKTL CV.PCPDY.SYTDSW
TNFR profile  | |. ... |. | | | : | | : | | : |. | .
              6 YHYDQNGRMCEECHMCQPGHFLVKHCKQPKRDTVCHKPCEPGVTYTTDDW
FRI-1  116 H
TNFR profile  |
              56 H
Z Score = 8.29
```

FIG. 1C

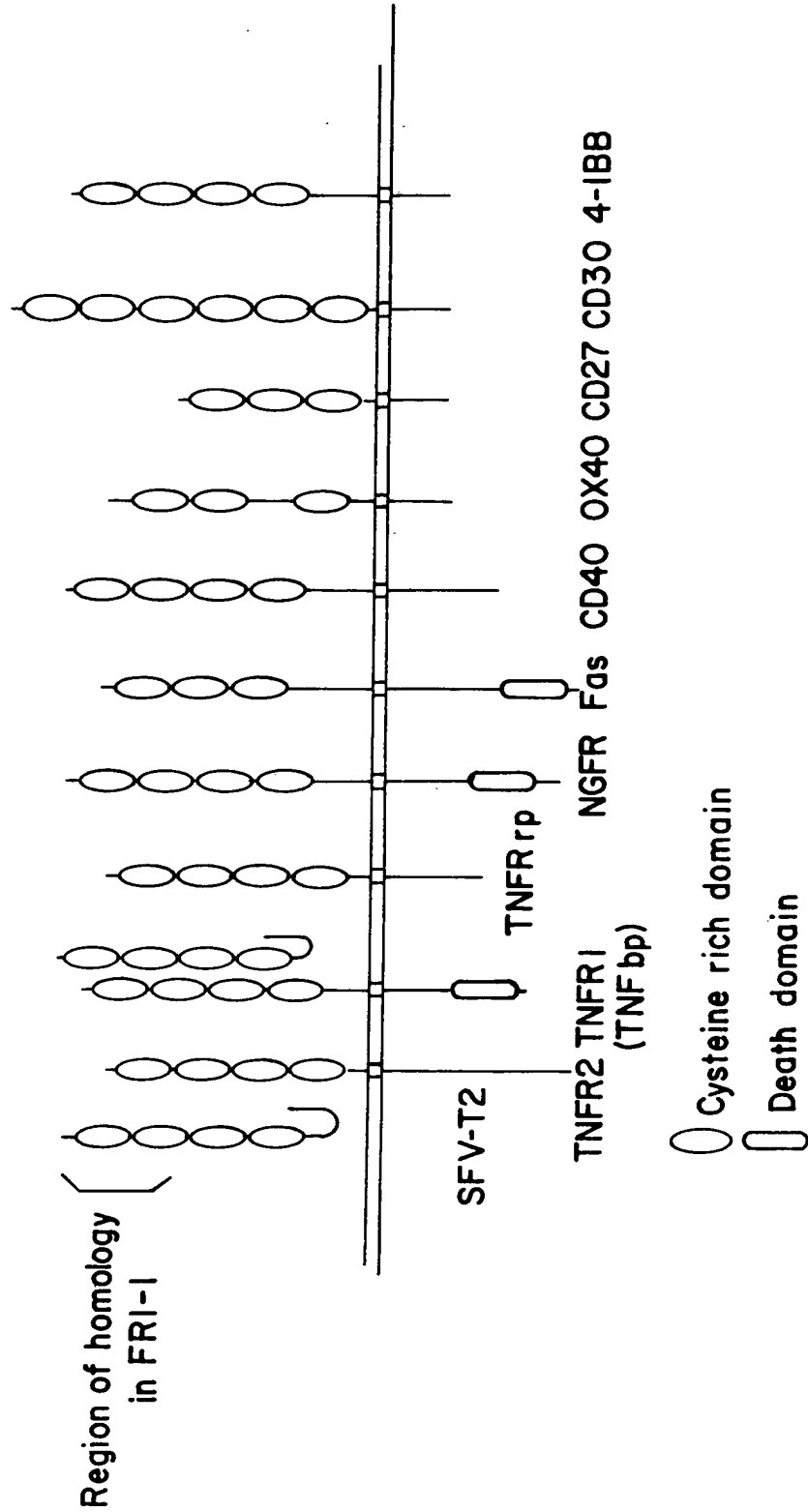


FIG.2A

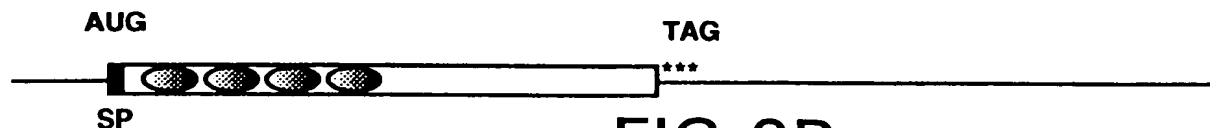


FIG.2B

10 30 50
ATCAAAGGCAGGGCATACTTCCTGTTGCCAGACCTTATATAAAACGTCATGTTTCGCCTG
70 90 110
GGCAGCAGAGAAGCACCTAGCACTGGCCCAGCGGCTGCCGCTGAGGTTTCCAGAGGACC
130 150 170
ACAATGAACAAGTGGCTGTGCTGTGCACTCCTGGTGTCTTGGACATCATTTGAATGGACA
M N K W L C C A L L V F L D I I E W T
190 210 230
ACCCAGGAAACCTTTCCTCCAAAATACTTGCATTATGACCCAGAAACCGGACGTCAGCTC
T O E T F P P K Y L H Y D P E T G R Q L
250 270 290
TTGTGTGACAAATGTGCTCCTGGCACCTACCTAAAACAGCACTGCACAGTCAGGAGGAAG
L C D K C A P G T Y L K Q H C T V R R K
310 330 350
ACACTGTGTGTCCCTTGCCCTGACTACTCTTATACAGACAGCTGGCACACGAGTGATGAA
T L C V P C P D Y S Y T D S W H T S D E
370 390 410
TGCGTGTACTGCAGCCCCGTGTGCAAGGAACTGCAGACCGTGAAACAGGAGTGCAACCGC
C V Y C S P V C K E L Q T V K Q E C N R
430 450 470
ACCCACAACCGAGTGTGCGAATGTGAGGAAGGGCGCTACCTGGAGCTCGAATTCTGCTTG
T H N R V C E C E E G R Y L E L E F C L
490 510 530
AAGCACCGGAGCTGTCCCCCAGGCTTGGGTGTGCTGCAGGCTGGGACCCCAGAGCGAAAC
K H R S C P P G L G V L Q A G T P E R N
550 570 590
ACGGTTTGCAAAAGATGTCCGGATGGGTTCTTCTCAGGTGAGACGTCATCGAAAGCACCC
T V C K R C P D G F F S G E T S S K A P
610 630 650
TGTAGGAAACACACCAACTGCAGCTCACTTGGCCTCCTGCTAATTCAGAAAGGAAATGCA
C R K H T N C S S L G L L L I Q K G N A
670 690 710
ACACATGACAATGTATGTTCCGGAAACAGAGAAGCAACTCAAAATTGTGGAATAGATGTC
T H D N V C S G N R E A T Q N C G I D V
730 750 770
ACCTGTGCGAAGAGGCATTCTTCAGGTTTGCTGTGCCTACCAAGATTATACCGAATTGG
T L C E E A F F R F A V P T K I I P N W
790 810 830
CTGAGTGTTCTGGTGGACAGTTTGCCTGGGACCAAAGTGAATGCAGAGAGTGTAGAGAGG
L S V L V D S L P G T K V N A E S V E R
850 870 890
ATAAAACGGAGACACAGCTCGCAAGAGCAAACCTTCCAGCTACTTAAGCTGTGGAAGCAT
I K R R H S S Q E Q T F Q L L K L W K H
910 930 950
CAAAACAGAGACCAGGAAATGGTGAAGAAGATCATCCAAGACATTGACCTCTGTGAAAGC
Q N R D Q E M V K I I Q D I D L C E S
970 990 1010
AGTGTGCAACGGCATATCGGCCACGCGAACCTCACACAGAGCAGCTCCGCATCTTGATG
S V Q R H I G H A N L T T E Q L R I L M

FIG.2C

1030 1050 1070
GAGAGCTTGCCTGGGAAGAAGATCAGCCCAGACGAGATTGAGAGAACGAGAAAGACCTGC
E S L P G K K I S P D E I E R T R K T C
1090 1110 1130
AAACCCAGCGAGCAGCTCCTGAAGCTACTGAGCTTGTGGAGGATCAAAAATGGAGACCAA
K P S E Q L L K L L S L W R I K N G D Q
1150 1170 1190
GACACCTTGAAGGGCCTGATGTACGCACTCAAGCACTTGAAAGCATACCACTTTCCCAA
D T L K G L M Y A L K H L K A Y H F P K
1210 1230 1250
ACCGTCACCCACAGTCTGAGGAAGACCATCAGGTTCTTGACACAGCTTCACCATGTACCGA
T V T H S L R K T I R F L H S F T M Y R
1270 1290 1310
TTGTATCAGAACTCTTTCTAGAAATGATAGGGAATCAGGTTCAATCAGTGAAGATAAGC
L Y Q K L F L E M I G N Q V Q S V K I S
1330 1350 1370
TGCTTATAGTTAGGAATGGTCACTGGGCTGTTTCTTCAGGATGGGCCAACACTGATGGAG
C L
1390 1410 1430
CAGATGGCTGCTTCTCCGGCTCTTGAAATGGCAGTTGATTCCTTTCTCATCAGTTGGTGG
1450 1470 1490
GAATGAAGATCCTCCAGCCCAACACACACACTGGGGAGTCTGAGTCAGGAGAGTGAGGCA
1510 1530 1550
GGCTATTTGATAATTGTGCAAAGCTGCCAGGTGTACACCTAGAAAGTCAAGCACCCCTGAG
1570 1590 1610
AAAGAGGATATTTTTATAACCTCAAACATAGGCCCTTTCCTTCCTCTCCTTATGGATGAG
1630 1650 1670
TACTCAGAAGGCTTCTACTATCTTCTGTGTCATCCCTAGATGAAGGCCTCTTTTATTTAT
1690 1710 1730
TTTTTTTATTCCTTTTTTTTCGGAGCTGGGGACCGAACCCAGGGCCTTGCGCTTGCGAGGCAA
1750 1770 1790
GTGCTCTACCACTGAGCTAAATCTCCAACCCCTGAAGGCCTCTTTCTTTCTGCCTCTGAT
1810 1830 1850
AGTCTATGACATTCTTTTTTCTACAATTCGTATCAGGTGCACGAGCCTTATCCCATTGT
1870 1890 1910
AGGTTTCTAGGCAAGTTGACCGTTAGCTATTTTCCCTCTGAAGATTTGATTTCGAGTTGC
1930 1950 1970
AGACTTGGCTAGACAAGCAGGGGTAGGTATGGTAGTTTATTTAACAGACTGCCACCAGG
1990 2010 2030
AGTCCAGTGTTTCTTGTTCCCTCTGTAGTTGTACCTAAGCTGACTCCAAGTACATTTAGTA
2050 2070 2090
TGAAAAATAATCAACAAATTTTATTCCTTCTATCAACATTGGCTAGCTTTGTTTCAGGGC
2110 2130 2150
ACTAAAAGAACTACTATATGGAGAAAGAATTGATATTGCCCCCAACGTTCAACAACCCA
2170 2190 2210
ATAGTTTATCCAGCTGTCATGCCTGGTTCAGTGTCTACTGACTATGCGCCCTCTTATTAC
2230 2250 2270
TGCATGCAGTAATTCAACTGGAAATAGTAATAATAATAATAGAAATAAAATCTAGACTCC
2290 2310 2330
ATTGGATCTCTCTGAATATGGGAATATCTAACTTAAGAAGCTTTGAGATTTTCAGTTGTGT
2350 2370 2390
TAAAGGCTTTTATTAAAAAGCTGATGCTCTTCTGTAAAAGTTACTAATATATCTGTAAGA
2410 2430
CTATTACAGTATTGCTATTTATATCCATCCAG

FIG. 2D

fas.frg	M L G I W T - - - L L P L V L T S - V A R L S S K S V N A Q V T D I N S K G L E L R K K T V T T V E	45
tnfr1.frg	- M G L S T V P D L L L P L V L L E L L V G I Y P S G V I G L V P H - - - L L G D R E K R D S V C	44
sfv-t2.frg	- - - - - - - - - - - M L R L I A L L V C V V Y V Y G D D V P Y S S N Q	25
tnfr2.frg	- - - - - - - M A P V A V W A A L A V G L E L W A A H A L P A Q V A F T P Y A P E P G S T	39
cd40.frg	- - - - - - - - - - - M V S L P R L C A L W L G C L L T A V H L G Q C V T C S D	28
osteo.frg	- - - - - - - - - - - M N K W L C C A L L V F L D I I E W T T Q E T F P P	26
ngfr.frg	- - - - - - - M G A G A T G R A M D G P R L L L L L G V S L L G - G A K E A C P T	34
ox40.frg	- - - - - - - - - - - M Y V W V Q Q P T A E L L L G L S L L G V T V K L N C V K	28
4lbb.frg	- - - - - - - - - - - M G N N C Y N V V I V L L L V G C C E K V G A V Q	25

fas.frg	T	Q	N	L	E	G	L	H	H	D	G	Q	Q	F	C	H	K	K	P	C	P	P	G	E	R	K	A	R	D	C	T	V	N	G	D	E	P	D	C	V	P	C	Q	E	G	K	E	Y	T	D	K	A	95	
tnfr1.frg	P	Q	G	K	Y	I	H	P	Q	N	N	S	I	C	C	C	C	A	S	K	C	C	H	K	G	T	Y	L	N	D	C	G	P	G	G	Q	D	T	D	C	R	E	C	S	G	S	F	T	A	S	E	N	94	
sfv-t2.frg	G	K	C	G	G	H	D	Y	E	K	D	G	L	C	C	C	S	P	G	G	C	C	H	P	G	F	Y	A	S	R	L	C	T	S	D	T	V	C	D	S	P	C	-	E	D	S	F	T	A	S	T	N	74	
tnfr2.frg	C	R	L	R	E	Y	Y	D	Q	T	A	Q	M	C	C	C	S	R	L	T	S	H	C	Q	Q	Q	H	A	K	V	F	C	T	A	L	E	K	T	V	C	D	S	E	D	S	F	T	Q	L	W	N	88		
cd40.frg	K	Q	Y	L	H	D	G	Q	C	-	-	-	-	-	-	C	D	L	C	A	C	A	P	P	G	S	R	L	T	S	H	C	T	A	L	E	K	T	V	C	D	S	E	D	S	F	T	Q	L	W	N	72		
osteo.frg	K	Y	L	H	Y	D	P	E	T	G	R	Q	L	L	L	C	C	K	A	C	N	L	G	G	E	G	V	A	Q	P	C	T	V	R	R	K	T	L	C	C	H	P	C	-	P	D	Y	S	T	D	S	W	H	75
ngfr.frg	G	L	Y	T	H	S	G	E	-	-	-	-	-	-	-	C	C	K	A	C	N	L	G	G	E	G	V	A	Q	P	C	T	V	R	R	K	T	L	C	C	H	P	C	-	P	D	Y	S	T	D	S	W	H	78
ox40.frg	D	T	Y	P	S	G	H	K	-	-	-	-	-	-	-	C	C	K	A	C	N	L	G	G	E	G	V	A	Q	P	C	T	V	R	R	K	T	L	C	C	H	P	C	-	P	D	Y	S	T	D	S	W	H	72
4lbb.frg	N	-	-	-	-	-	-	-	-	-	-	-	-	-	-	S	C	D	N	C	Q	P	P	G	E	R	K	A	R	D	C	T	V	N	G	D	E	P	D	C	V	P	C	Q	E	G	K	E	Y	T	D	K	A	54

[illegible]

FIG. 2E

[illegible][illegible][illegible]

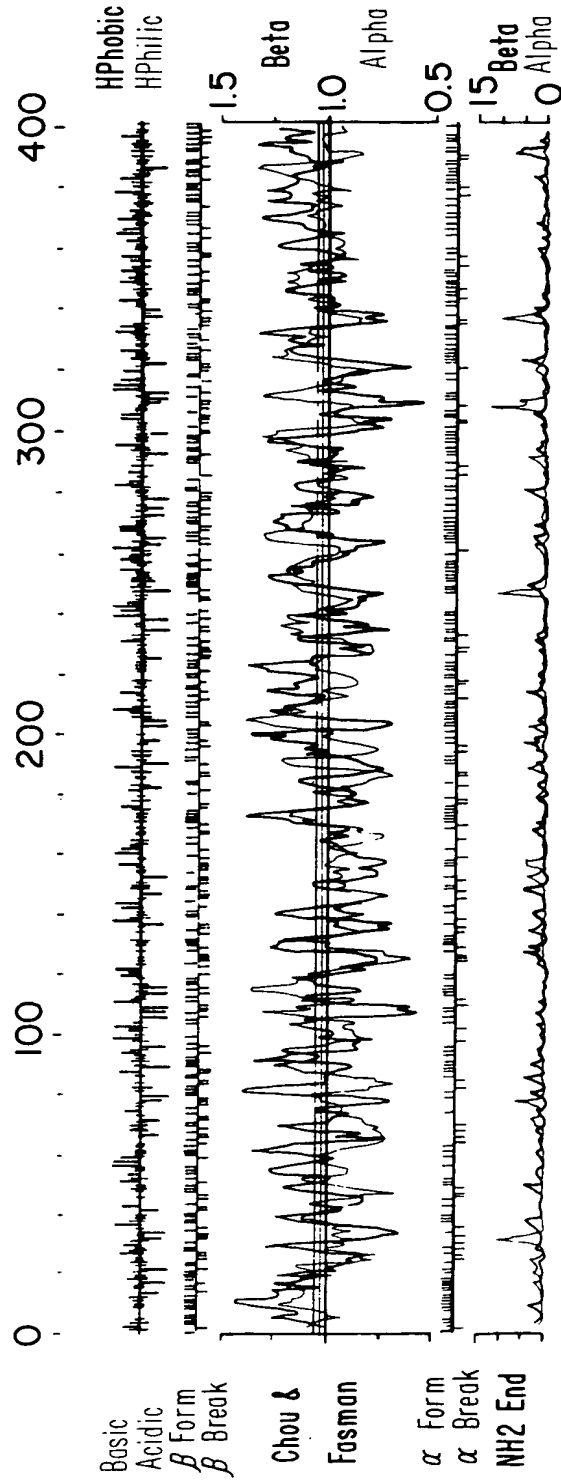


FIG. 3A

FIG. 3B

FIG. 3C

FIG. 3D

FIG. 3E

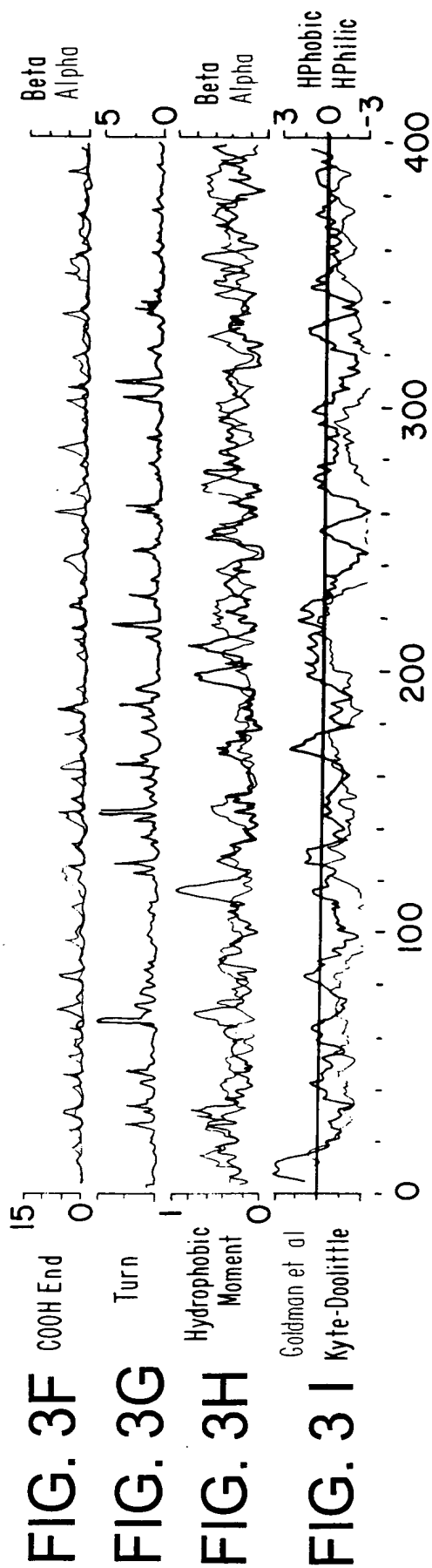


FIG.4A

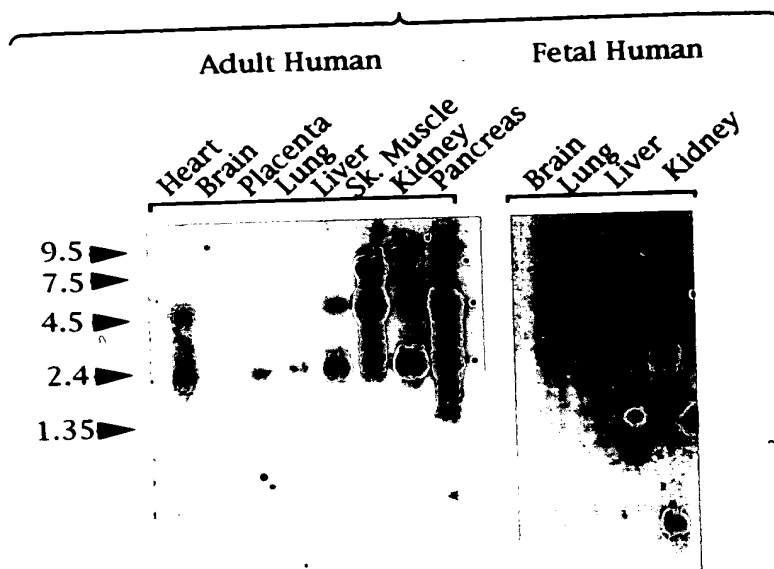


FIG.4B

Human Immune System

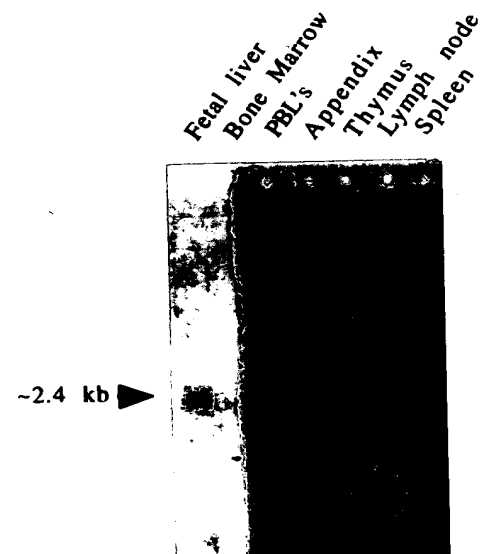


FIG. 5

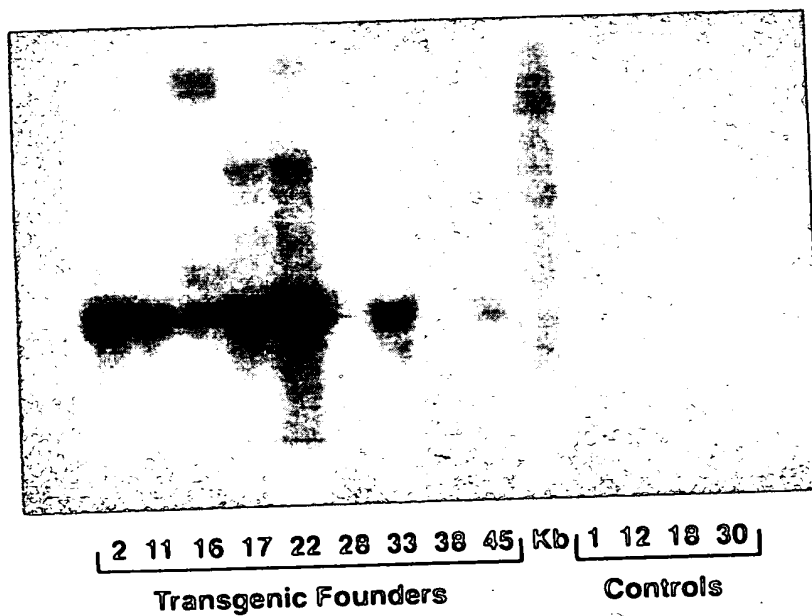


FIG.6A

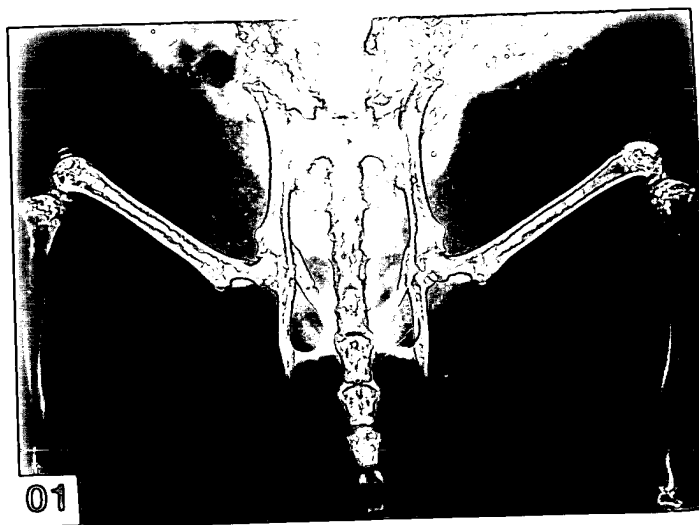


FIG.6B

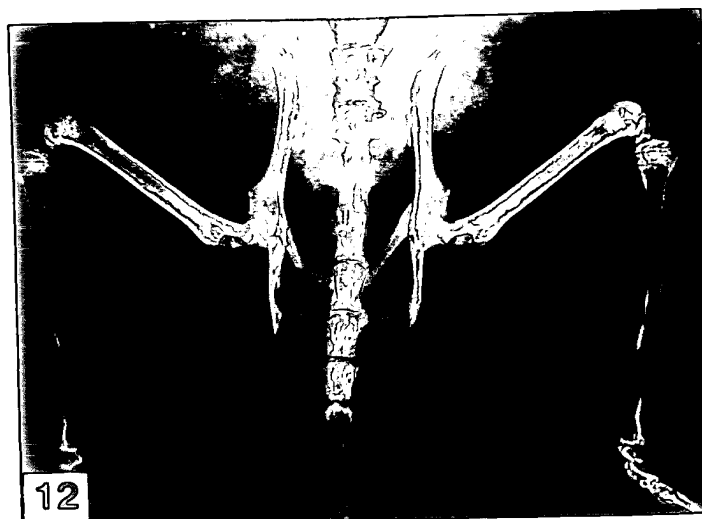


FIG.6C

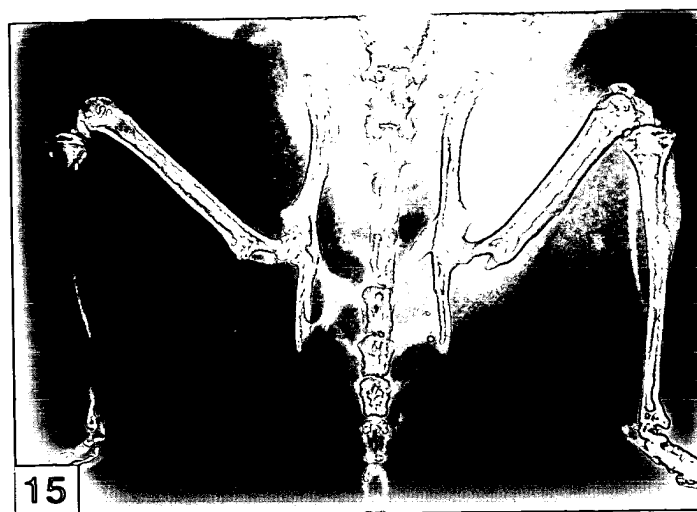


FIG. 6D

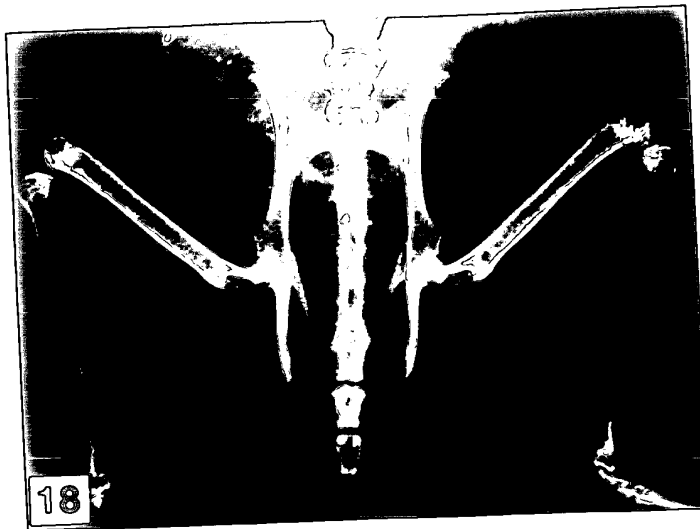


FIG. 6E



FIG. 6F

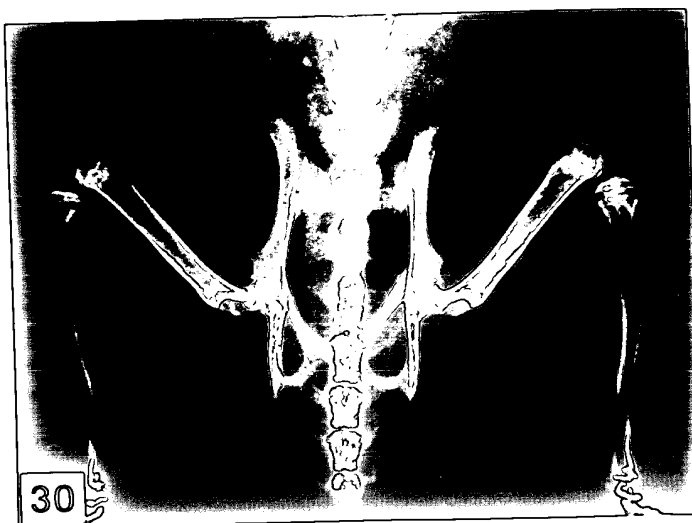


FIG. 6G



FIG. 6H

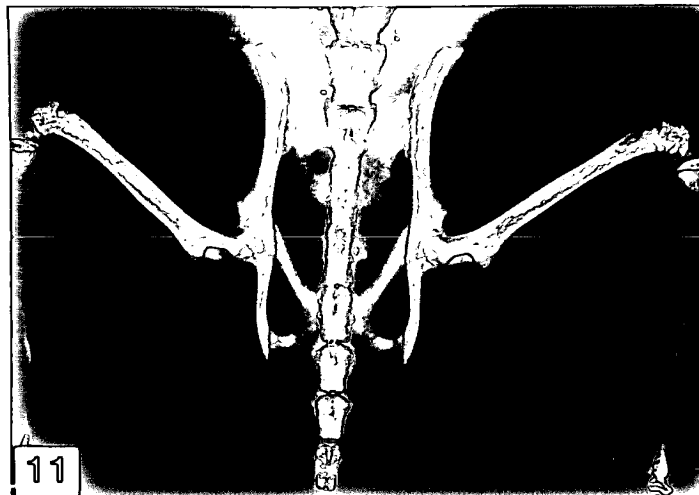


FIG. 6I

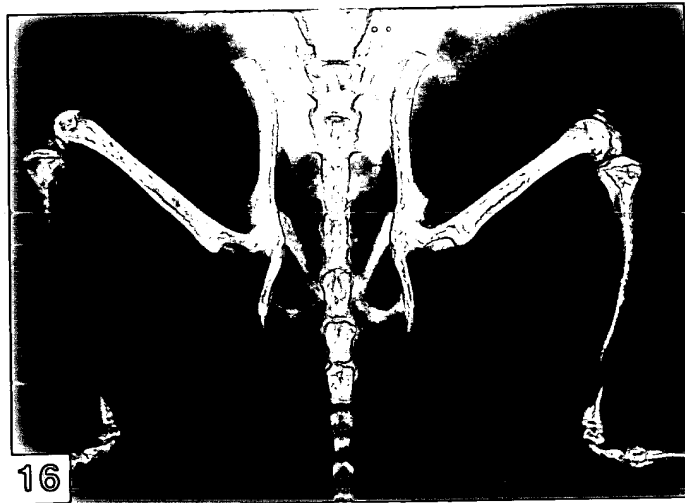


FIG. 6J

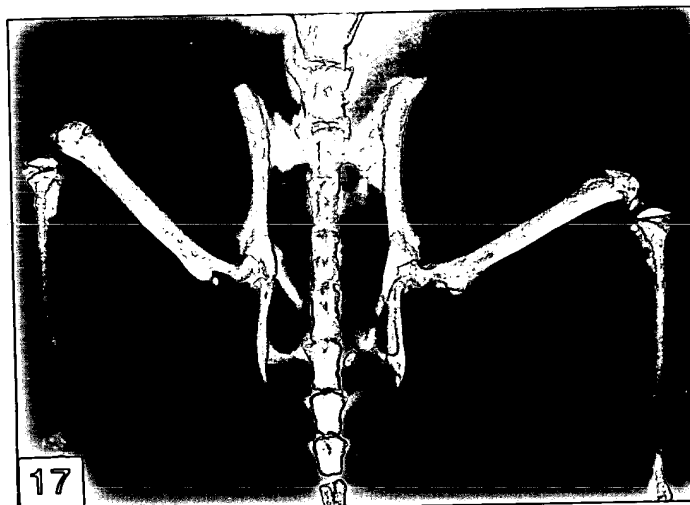


FIG. 7A

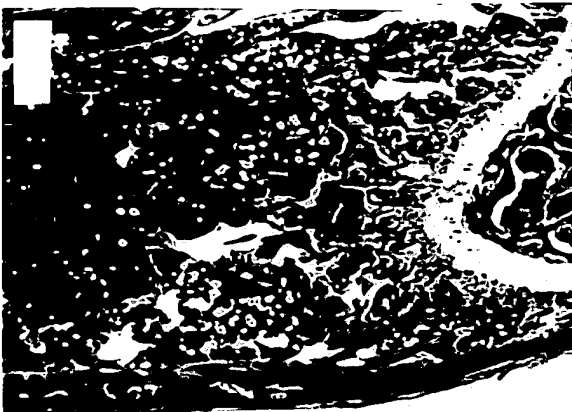


FIG. 7B

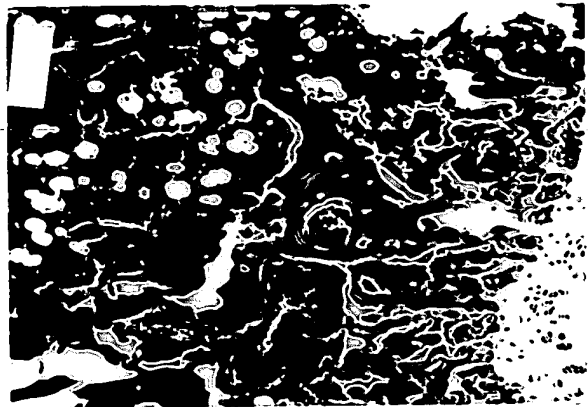


FIG. 7C



FIG. 7D

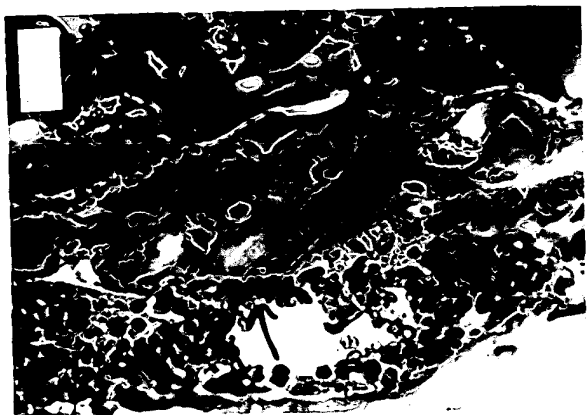


FIG. 7E

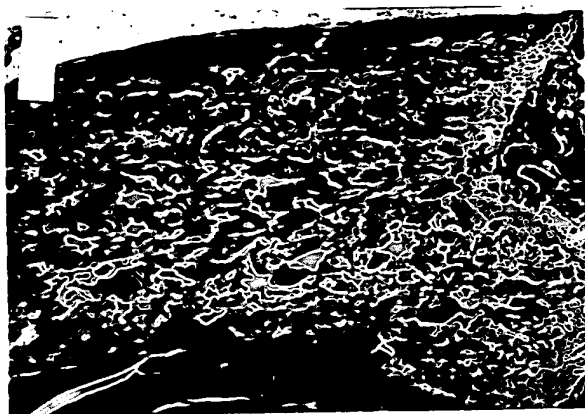


FIG. 7F

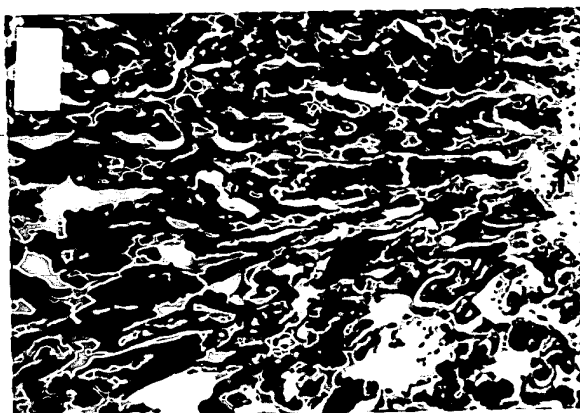


FIG. 7G

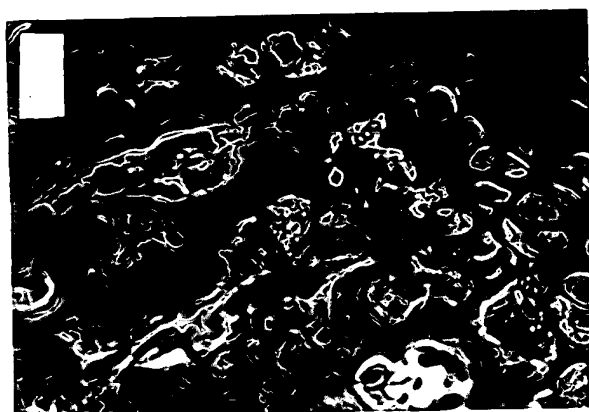


FIG. 7H

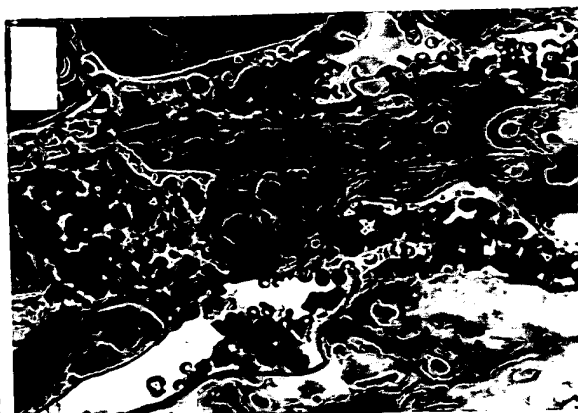


FIG.8A



FIG.8B

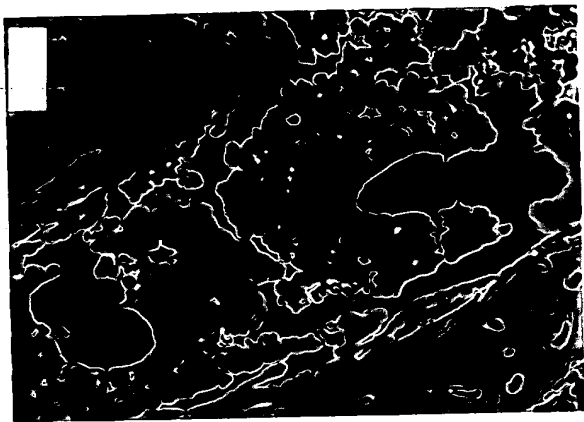


FIG.8C

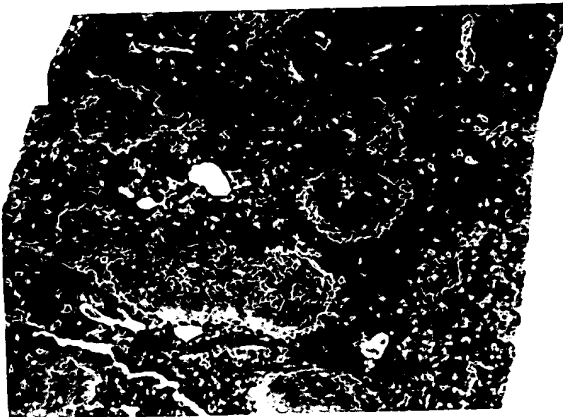


FIG.8D

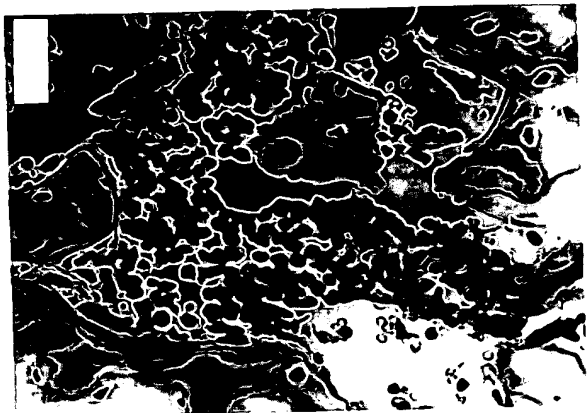


FIG.9A

10 30 50
CCTTATATAARACGTCATGATTGCCTGGGCTGCAGAGACGCACCTAGCACTGACCCAGCG
70 90 110
GCTGCCTCCTGAGGTTTCCCGAGGACCACAATGAACAAGTGGCTGTGCTGCGCACTCCTG
M N K W L C C A L L
130 150 170
GTGCTCCTGGACATCATTTGAATGGACAACCCAGGAAACCCTTCCTCCAAAGTACTTGCAT
V L L D I I E W T T O E T L P P K Y L H
190 210 230
TATGACCCAGAACTGGTCATCAGCTCCTGTGTGACAAATGTGCTCCTGGCACCTACCTA
Y D P E T G H Q L L C D K C A P G T Y L
250 270 290
AAACAGCACTGCACAGTGAGGAGGAAGACATTGTGTGTCCCTTGCCCTGACCACTCTTAT
K Q H C T V R R K T L C V P C P D H S Y
310 330 350
ACGGACAGCTGGCACACCAGTGATGAGTGTGTGTATTGCAGCCCAGTGTGCAAGGAAGT
T D S W H T S D E C V Y C S P V C K E L
370 390 410
CAGTCCGTGAAGCAGGAGTGCAACCGCACCCACAACCGAGTGTGTGAGTGTGAGGAAGGG
Q S V K Q E C N R T H N R V C E C E E G
430 450 470
CGTTACCTGGAGATCGAATTCTGCTTGAAGCACCGGAGCTGTCCCCGGGCTCCGGCGTG
R Y L E I E F C L K H R S C P P G S G V
490 510 530
GTGCAAGCTGGAACCCAGAGCGAAACACAGTTTGCAAAAAATGTCCAGATGGGTTCTTC
V Q A G T P E R N T V C K K C P D G F F
550 570 590
TCAGGTGAGACTTCATCGAAAGCACCCCTGTATAAAACACACGAACTGCAGCACATTGCGC
S G E T S S K A P C I K H T N C S T F G
610 630 650
CTCCTGCTAATTCAGAAAGGAAATGCAACACATGACAACGTGTGTTCCGGAAACAGAGAA
L L L I Q K G N A T H D N V C S G N R E
670 690 710
GCCACGCAAAAGTGTGGAATAGATGTCACCCTGTGTGAAGAGGCCTTCTTCAGGTTTGCT
A T Q K C G I D V T L C E E A F F R F A
730 750 770
GTTCTACCAAGATTATACCAAATTGGCTGAGTGTGTTTGGTGGACAGTTTGCCTGGGACC
V P T K I I P N W L S V L V D S L P G T

FIG.9B

790 810 830
AAAGTGAATGCCGAGAGTGTAGAGAGGATAAAACGGAGACACAGCTCACAAAGAGCAAACC
K V N A E S V E R I K R R H S S Q E Q T
850 870 890
TTCCAGCTGCTGAAGCTGTGGAACATCAAAACAGAGACCAGGAAATGGTGAAGAAGATC
F Q L L K L W K H Q N R D Q E M V K K I
910 930 950
ATCCAAGACATTGACCTCTGTGAAAGCAGCGTGCAGCGGCATCTCGGCCACTCGAACCTC
I Q D I D L C E S S V Q R H L G H S N L
970 990 1010
ACCACAGAGCAGCTTCTTGCCTTGATGGAGAGCCTGCCTGGGAAGAAGATCAGCCCAGAA
T T E Q L L A L M E S L P G K K I S P E
1030 1050 1070
GAGATTGAGAGAACGAGAAAGACCTGCAAATCGAGCGAGCAGCTCCTGAAGCTACTCAGT
E I E R T R K T C K S S E Q L L K L L S
1090 1110 1130
TTATGGAGGATCAAAAATGGT'GACCAAGACACCTTGAAGGGCCTGATGTATGCCCTCAAG
L W R I K N G D Q D T L K G L M Y A L K
1150 1170 1190
CACTTGAAAACATCCCCTTT'CCCCAAAAGTGTACCCACAGTCTGAGGAAGACCATGAGG
H L K T S H F P K T V T H S L R K T M R
1210 1230 1250
TTCCTGCACAGCTTCACAATGTACAGACTGTATCAGAAGCTCTTTTTAGAAATGATAGGG
F L H S F T M Y R L Y Q K L F L E M I G
1270 1290 1310
AATCAGGTTCAATCCGTGAAAATAAGCTGCTTATAACTAGGAATGGTCACTGGGCTGTTT
N Q V Q S V K I S C L

CTTCA

FIG.9C

10 30 50
GTATATATAACGTGATGAGCGTACGGGTGCGGAGACGCACCGGAGCGCTCGCCCAGCCGC
70 90 110
CGYCTCCAAGCCCCCTGAGGTTTCCGGGGACCACAATGAACAAGTTGCTGTGCTGCGCGCT
M N K L L C C A L
130 150 170
CGTGTTTCTGGACATCTCCATTAAAGTGGACCACCCAGGAAACGTTTCCTCCAAAGTACCT
V F L D I S I K W T T O E T F P P K Y L
190 210 230
TCATTATGACGAAGAAACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTA
H Y D E E T S H Q L L C D K C P P G T Y
250 270 290
CCTAAAACAACACTGTACAGCAAAGTGGAAGACCGTGTGCGCCCCTTGCCCTGACCACTA
L K Q H C T A K W K T V C A P C P D H Y
310 330 350
CTACACAGACAGCTGGCACACCAAGTGACGAGTGTCTATACTGCAGCCCCGTGTGCAAGGA
Y T D S W H T S D E C L Y C S P V C K E
370 390 410
GCTGCAGTACGTCAAGCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGGA
L Q Y V K Q E C N R T H N R V C E C K E
430 450 470
AGGGCGCTACCTTGAGATAGAGTTCTGCTTGAAACATAGGAGCTGCCCTCCTGGATTG
G R Y L E I E F C L K H R S C P P G F G
490 510 530
AGTGGTGCAAGCTGGAACCCAGAGCGAAATACAGTTTGCAAAGATGTCCAGATGGGTT
V V Q A G T P E R N T V C K R C P D G F
550 570 590
CTTCTCAAATGAGACGTCATCTAAAGCACCCCTGTAGAAAACACACAAATTGCAGTGTCTT
F S N E T S S K A P C R K H T N C S V F
610 630 650
TGGTCTCCTGCTAACTCAGAAAGGAAATGCAACACACGACAACATATGTTCCGGAAACAG
G L L L T Q K G N A T H D N I C S G N S
670 690 710
TGAATCAACTCAAAAATGTGGAATAGATGTTACCCTGTGTGAGGAGGCATTCTTCAGGTT
E S T Q K C G I D V T L C E E A F F R F
730 750 770
TGCTGTTCCCTACAAAGTTTACGCCTAACTGGCTTAGTGTCTTGGTAGACAATTTGCCTGG
A V P T K F T P N W L S V L V D N L P G

FIG.9D

790 810 830
CACCAAAGTAAACGCAGAGAGTGTAGAGAGGATAAAACGGCAACACAGCTCACAGAACA
T K V N A E S V E R I K R Q H S S Q E Q
850 870 890
GACTTTCAGCTGCTGAAGTTATGGAAACATCAAACAAAGACCAAGATATAGTCAAGAA
T F Q L L K L W K H Q N K D Q D I V K K
910 930 950
GATCATCCAAGATATTGACCTCTGTGAAAACAGCGTGCAGCGGCACATTGGACATGCTAA
I I Q D I D L C E N S V Q R H I G H A N
970 990 1010
CCTCACCTTCGAGCAGCTTCGTAGCTTGATGGAAAGCTTACCGGGAAAGAAAGTGGGAGC
L T F E Q L R S L M E S L P G K K V G A
1030 1050 1070
AGAAGACATTGAAAAACAATAAAGGCATGCAAACCCAGTGACCAGATCCTGAAGCTGCT
E D I E K T I K A C K P S D Q I L K L L
1090 1110 1130
CAGTTTGTGGCGAATAAAAAATGGCGACCAAGACACCTTGAAGGGCCTAATGCACGCACT
S L W R I K N G D Q D T L K G L M H A L
1150 1170 1190
AAAGCACTCAAAGACGTACCACTTTCCCAAAACTGTCACTCAGAGTCTAAAGAAGACCAT
K H S K T Y H F P K T V T Q S L K K T I
1210 1230 1250
CAGGTTTCCTTCACAGCTTCACAATGTACAAATTGTATCAGAAGTTATTTTGTAGAAATGAT
R F L H S F T M Y K L Y Q K L F L E M I
1270 1290 1310
AGGTAACCAGGTCCAATCAGTAAAAATAAGCTGCTTATAACTGGAAATGGCCATTGAGCT
G N Q V Q S V K I S C L
1330 1350
GTTTCCTCACAAATTGGCGAGATCCCATGGATGATAA

FIG. 9E

muosteo.frg	M N K W L C C A L L V L L D I I E W T T Q E T L P P K Y L H Y D P E T G H Q L L C D K K C A P G T Y L	50
ratosteo.frg	M N K W L C C A L L V F L D I I E W T T Q E T F P P K Y L H Y D P E T G R Q L L C D K K C A P G T Y L	50
huosteo.frg	M N K L L C C A L V F L D I S I K W T T Q E T F P P K Y L H Y D E E T S H Q L L C D K C P P G T Y L	50
muosteo.frg	K Q H C T V R R K T L C V P C P D H S Y T D S W H T S D E C V Y C S P V C K E L Q S V K Q E C N R T	100
ratosteo.frg	K Q H C T V R R K T L C V P C P D Y S Y T D S W H T S D E C V Y C S P V C K E L Q T V K Q E C N R T	100
huosteo.frg	K Q H C T A K W K T V C A P C P D H Y Y T D S W H T S D E C L Y C S P V C K E L Q Y V K Q E C N R T	100
muosteo.frg	H N R V C E C E E G R Y L E I E F C L K H R S C P P G S G V V Q A G T P E R N T V C K K C P D G F F	150
ratosteo.frg	H N R V C E C E E G R Y L E I E F C L K H R S C P P G L G V L Q A G T P E R N T V C K R C P D G F F	150
huosteo.frg	H N R V C E C K E G R Y L E I E F C L K H R S C P P G F G V V Q A G T P E R N T V C K R C P D G F F	150
muosteo.frg	S G E T S S K A P C I K H T N C S T F G L L L I Q K G N A T H D N V C S G N R E A T Q K C G I D V T	200
ratosteo.frg	S G E T S S K A P C R K H T N C S S L G L L L I Q K G N A T H D N V C S G N R E A T Q N C G I D V T	200
huosteo.frg	S N E T S S K A P C R K H T N C S V F G L L L T Q K G N A T H D N I C S G N S E S T Q K C G I D V T	200

FIG. 9F

muosteo.frg 250
ratosteo.frg 250
huosteo.frg 250

L	C	E	E	A	F	F	R	F	A	V	P	T	K	I	I	P	N	W	L	S	V	L	V	D	S	L	P	G	T	K	V	N	A	E	S	V	E	R	I	K	R	R	H	S	S	Q	E	Q	T
L	C	E	E	A	F	F	R	F	A	V	P	T	K	I	I	P	N	W	L	S	V	L	V	D	S	L	P	G	T	K	V	N	A	E	S	V	E	R	I	K	R	R	H	S	S	Q	E	Q	T
L	C	E	E	A	F	F	R	F	A	V	P	T	K	I	I	P	N	W	L	S	V	L	V	D	S	L	P	G	T	K	V	N	A	E	S	V	E	R	I	K	R	R	H	S	S	Q	E	Q	T

muosteo.frg 300
ratosteo.frg 300
huosteo.frg 300

F	Q	L	L	K	L	W	K	H	Q	N	R	D	Q	E	M	V	K	K	I	I	Q	D	I	D	L	C	E	S	S	V	Q	R	H	L	G	H	S	N	L	T	T	E	Q	L	L	A	L	M	E
F	Q	L	L	K	L	W	K	H	Q	N	R	D	Q	E	M	V	K	K	I	I	Q	D	I	D	L	C	E	S	S	V	Q	R	H	L	G	H	A	N	L	T	T	E	Q	L	L	I	L	M	E
F	Q	L	L	K	L	W	K	H	Q	N	R	D	Q	E	M	V	K	K	I	I	Q	D	I	D	L	C	E	S	S	V	Q	R	H	L	G	H	A	N	L	T	T	E	Q	L	L	S	L	M	E

muosteo.frg 350
ratosteo.frg 350
huosteo.frg 350

S	L	P	G	K	K	I	S	P	E	E	I	E	R	T	R	K	T	C	K	S	S	E	Q	L	L	K	L	L	S	L	W	R	I	K	N	G	D	Q	D	T	L	K	G	L	M	Y	A	L	K
S	L	P	G	K	K	I	S	P	E	E	I	E	R	T	R	K	T	C	K	P	S	E	Q	L	L	K	L	L	S	L	W	R	I	K	N	G	D	Q	D	T	L	K	G	L	M	Y	A	L	K
S	L	P	G	K	K	V	G	A	E	D	I	E	K	T	I	K	A	C	K	P	S	D	Q	I	L	K	L	L	S	L	W	R	I	K	N	G	D	Q	D	T	L	K	G	L	M	H	A	L	K

muosteo.frg 400
ratosteo.frg 400
huosteo.frg 400

H	L	K	T	S	H	F	P	K	T	V	T	H	S	L	R	K	T	M	R	F	L	H	S	F	T	M	Y	R	L	Y	Q	K	L	F	L	E	M	I	G	N	Q	V	Q	S	V	K	I	S	C
H	L	K	T	S	H	F	P	K	T	V	T	H	S	L	R	K	T	M	R	F	L	H	S	F	T	M	Y	R	L	Y	Q	K	L	F	L	E	M	I	G	N	Q	V	Q	S	V	K	I	S	C
H	S	K	T	Y	H	F	P	K	T	V	T	Q	S	L	K	K	T	I	R	F	L	H	S	F	T	M	Y	K	L	Y	Q	K	L	F	L	E	M	I	G	N	Q	V	Q	S	V	K	I	S	C

muosteo.frg 401
ratosteo.frg 401
huosteo.frg 401

L	L	L
---	---	---

FIG.10

1tnrr	C	P	Q	-	G	K	Y	I	H	P	Q	N	N	S	I	C	C	T	K	C	H	K	G	T	Y	L	Y	N	D	C	P	G	P	G	Q	D	T	C	R	E	C	E	S	G	S	F	T	A	S	49	
humoste	P	P	K	Y	L	H	Y	D	E	E	T	S	H	Q	L	L	C	D	K	C	P	P	G	T	Y	L	K	Q	H	C	T	A	K	-	W	K	T	V	C	A	P	C	P	D	H	Y	Y	T	D	S	49
1tnrr	E	N	H	L	R	H	C	L	S	C	S	-	K	C	R	K	E	M	G	Q	V	E	I	S	S	C	T	V	D	R	D	T	V	C	G	C	R	K	N	Q	Y	R	H	Y	W	S	E	N	L	F	98
humoste	W	H	T	S	D	E	C	L	Y	C	S	P	V	C	-	K	E	L	Q	Y	V	K	-	Q	E	C	N	R	T	H	N	R	V	C	E	C	K	E	G	R	Y	L	E	I	-	-	-	E	-	F	93
1tnrr	Q	C	F	N	C	S	L	C	L	N	G	-	T	V	H	L	S	C	Q	E	K	Q	N	T	V	C	T	-	C	H	A	G	F	F	L	R	E	-	-	-	N	E	C	V	S	C	139				
humoste	-	C	L	K	H	R	S	C	P	P	G	F	G	V	Q	A	G	T	P	E	R	N	T	V	C	K	R	C	P	D	G	F	F	S	N	E	T	S	S	K	A	P	C	R	K	H	139				

FIG. II

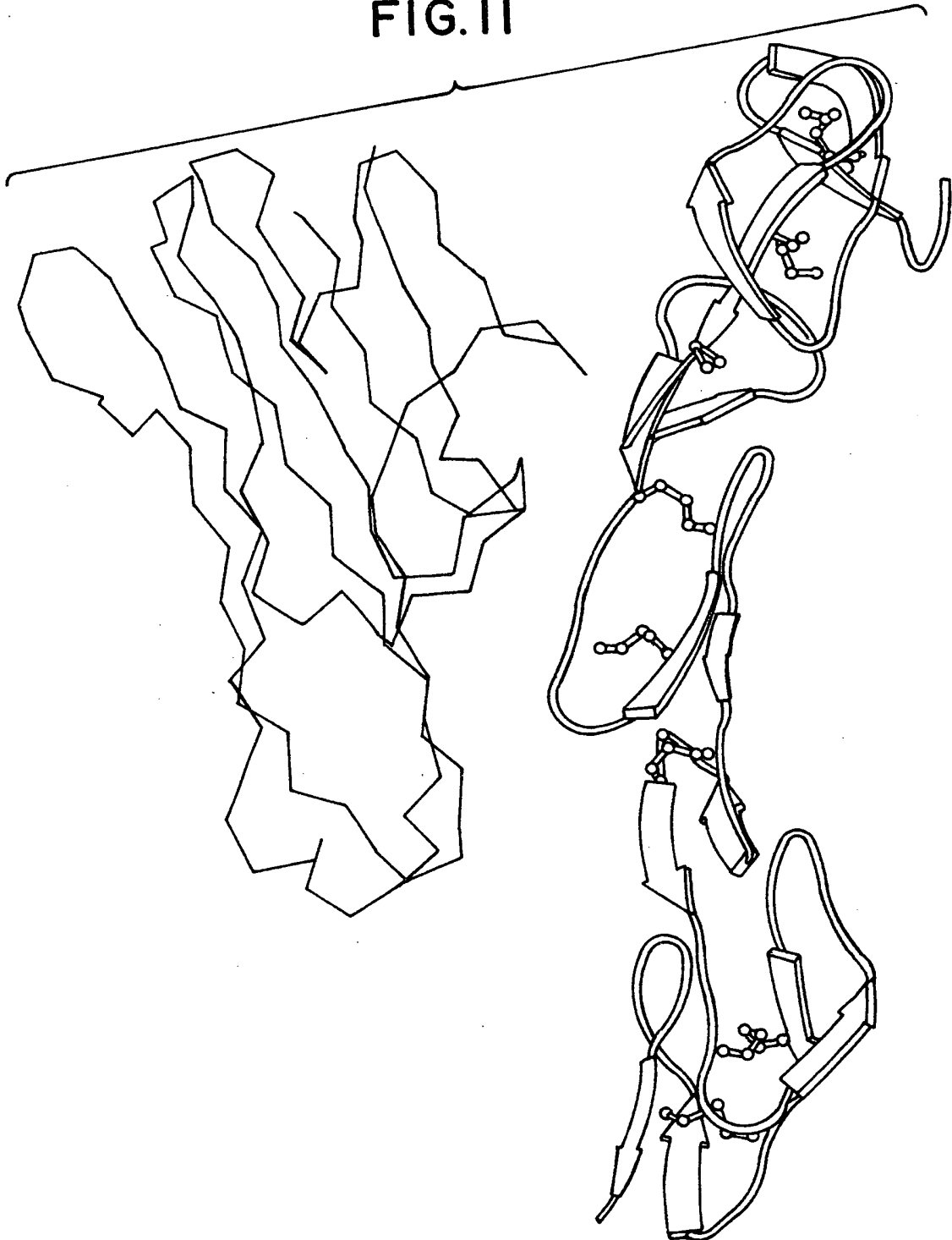


FIG. 12A

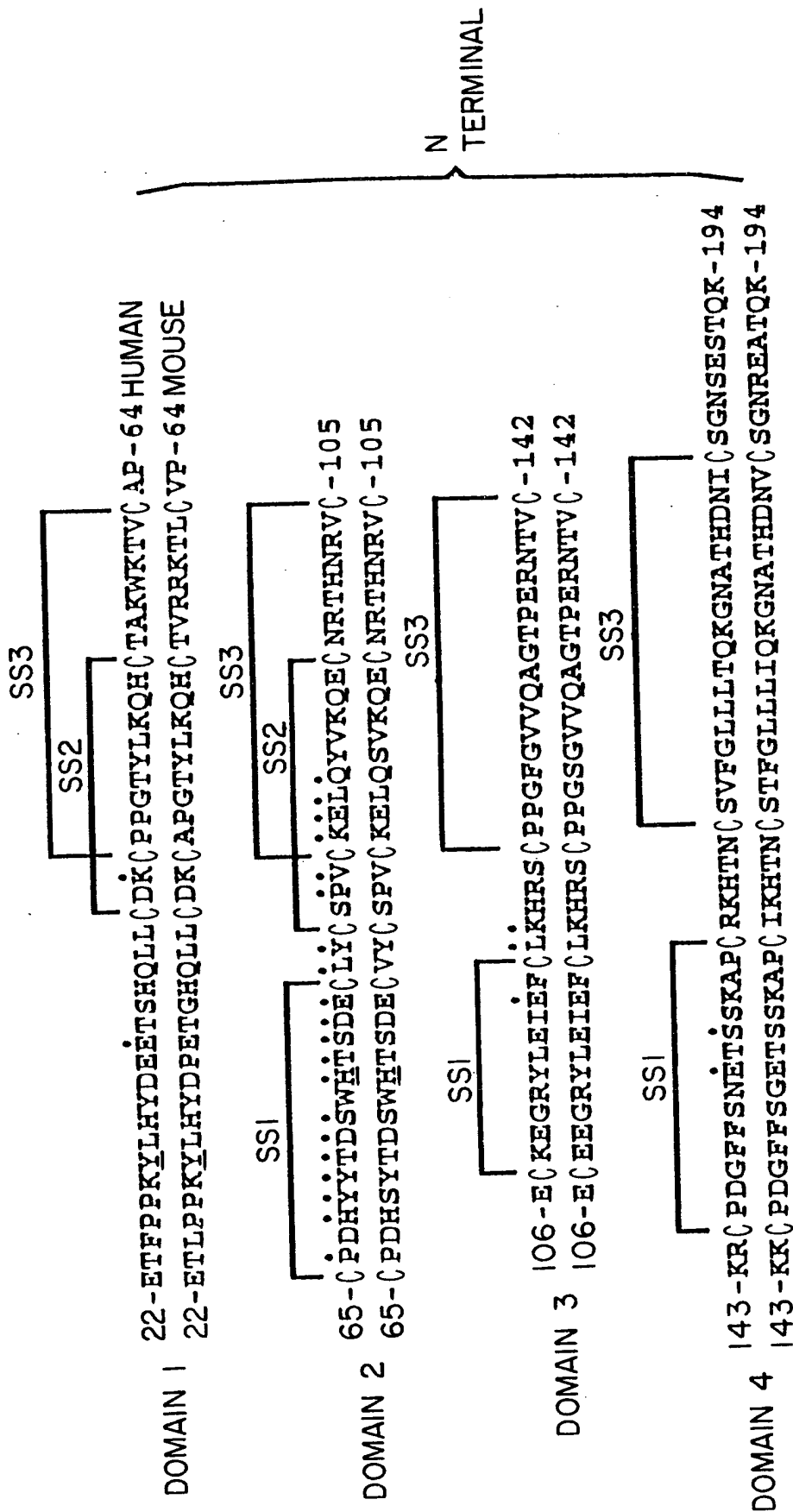


FIG. 12B

195 -CGIDVTLC^CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSS-246
195 -CGIDVTLC^CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRRHSS-246
247 -QEQTFFQLLKLWKHQNKDQDIVKKIIQDIDLC^CENSVQRHIGHANLTPEQLRSL-298
247 -QEQTFFQLLKLWKHQNRDQEMVKKIIQDIDLC^CESSVQRHLGHSNLTTEQLLAL-298
299 -MESLPGKKVGAEDIEKTIKAC^CKPSDQILKLLSLWRIKNGDQDTLKGLMHALK-350
299 -MESLPGKKISPEEIERTRKTC^CKSSEQLLKLLSLWRIKNGDQDTLKGLMYALK-350
351 -HSKTYHFPKTVTQSLKKTIRFLHSFTMYKLYQKLFLEMIGNQVQSVKISCL-401
351 -HLKTSHPKTVTHSLRKTRFLHSFTMYRLYQKLFLEMIGNQVQSVKISCL-401

C
TERMINAL

FIG. 13A

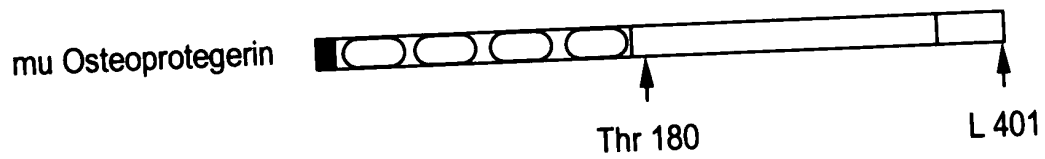


FIG. 13B

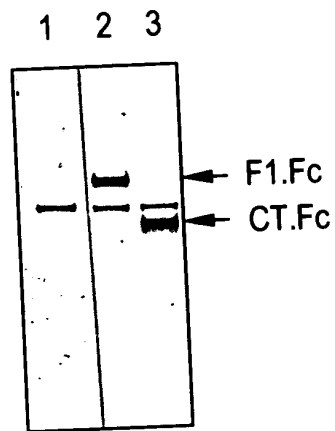


FIG. 13C

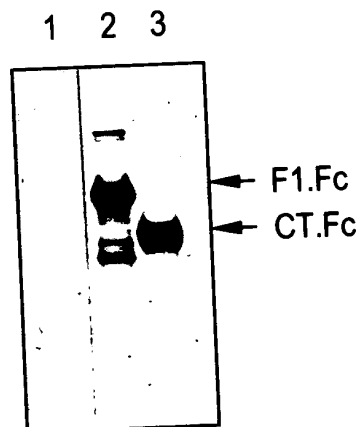


FIG.14A

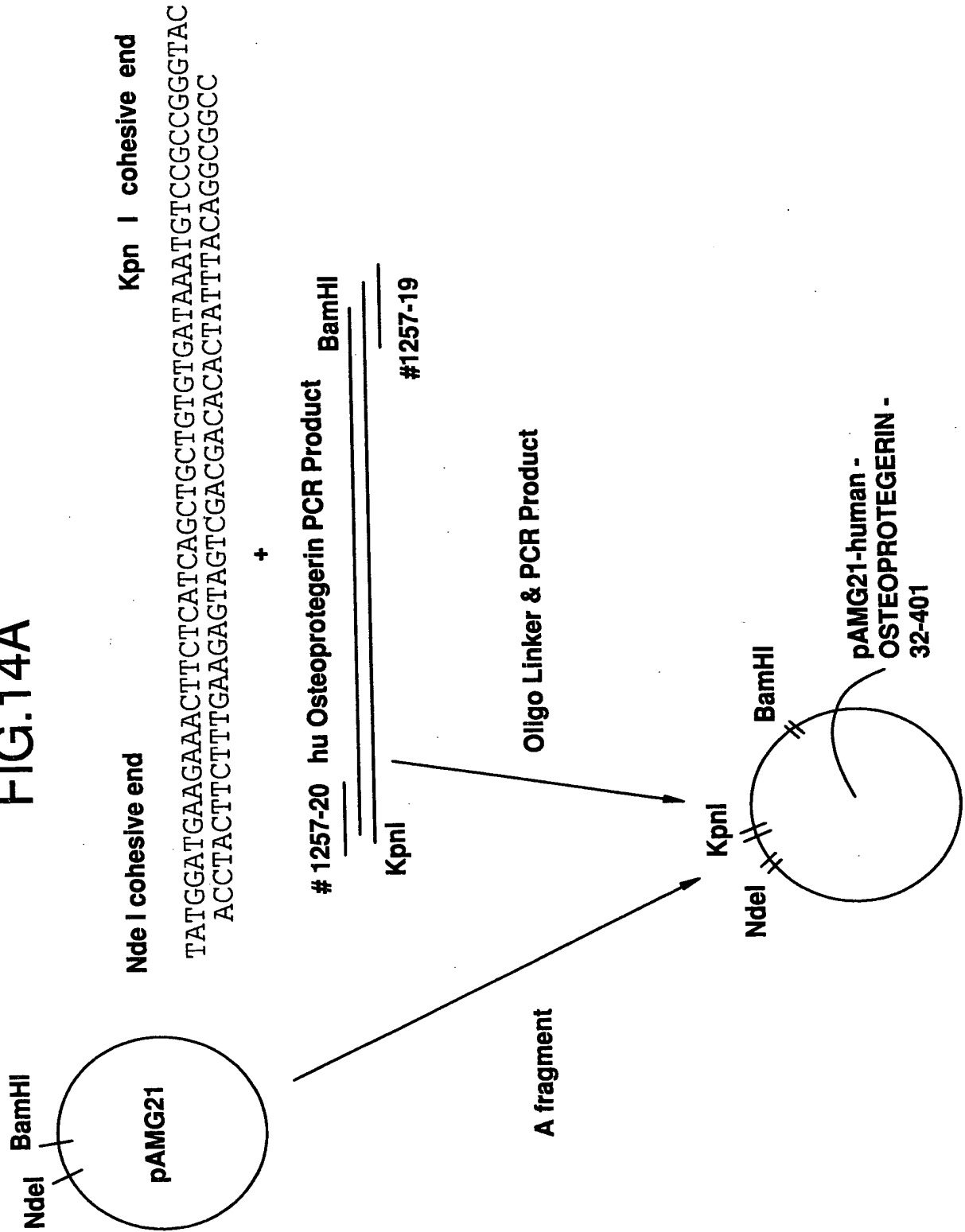


FIG. 14B

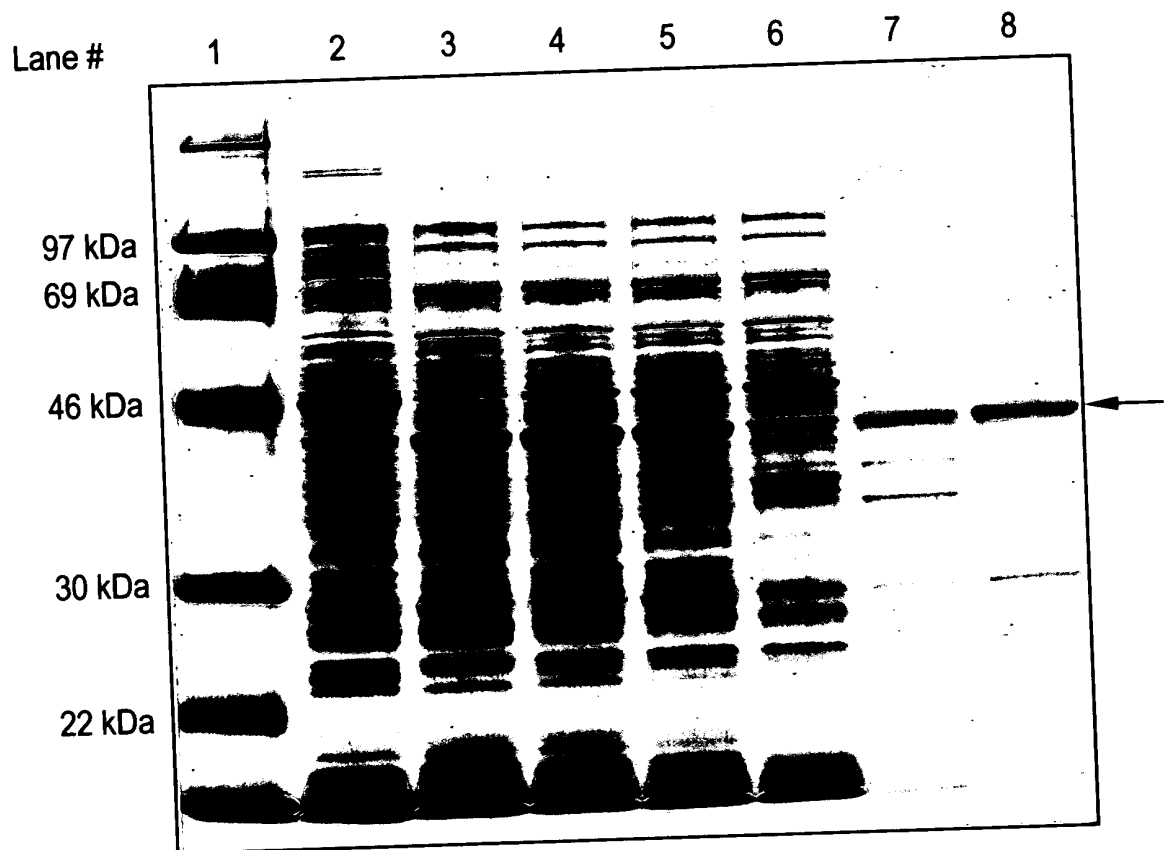


FIG. 15

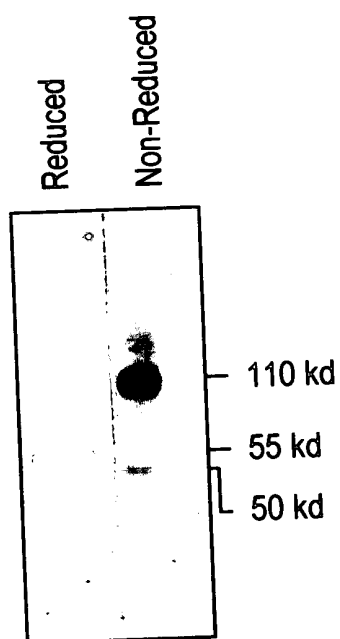


FIG. 16A

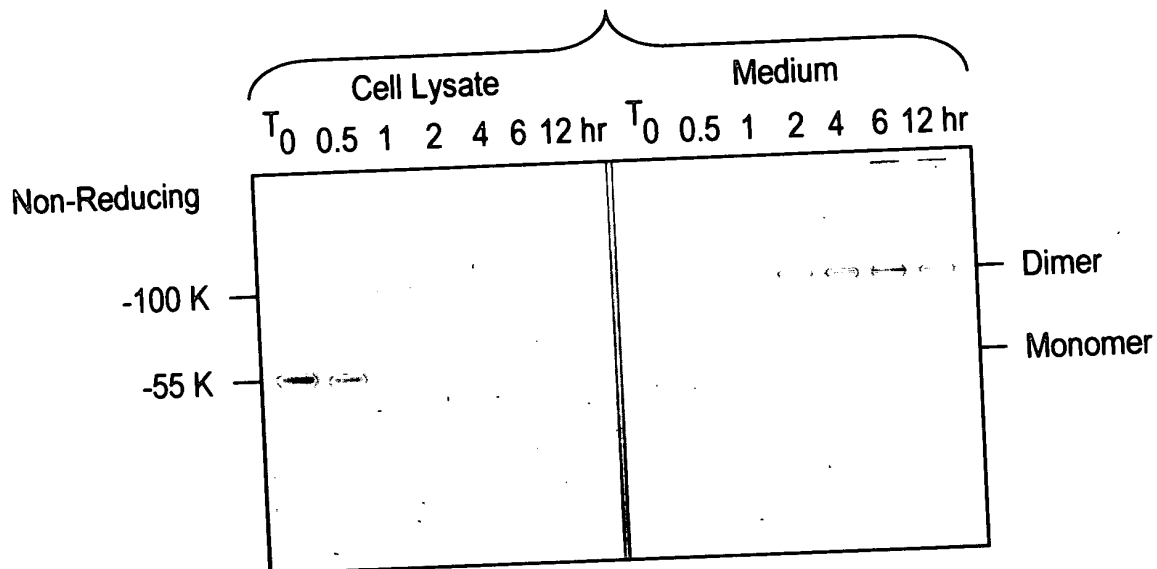


FIG. 16B

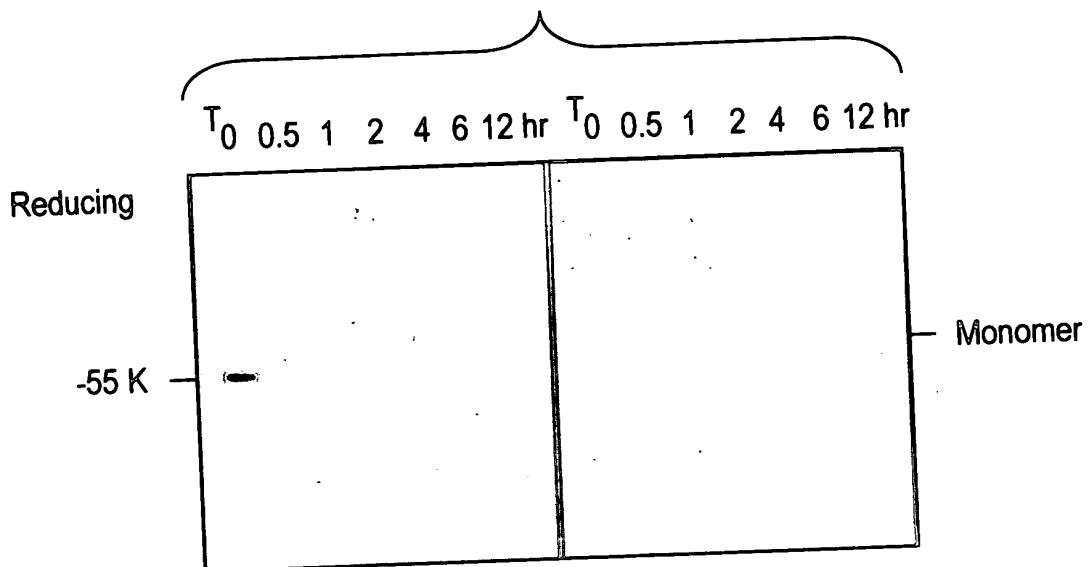


FIG. 17

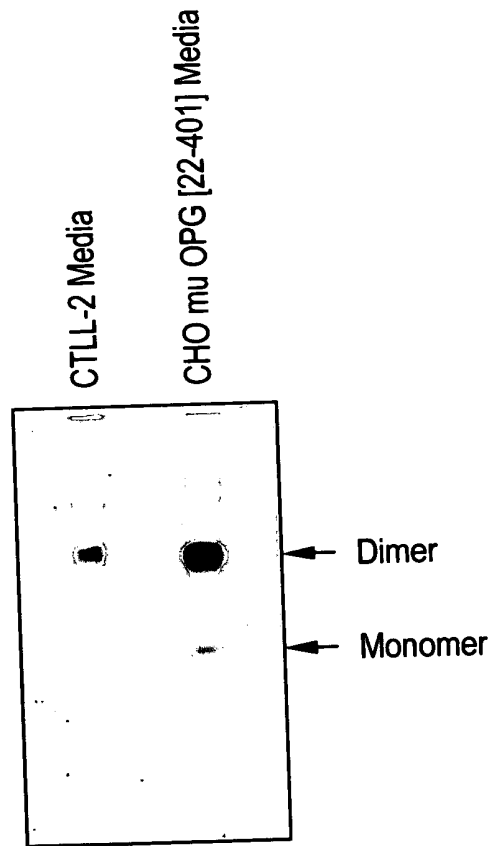


FIG. 18

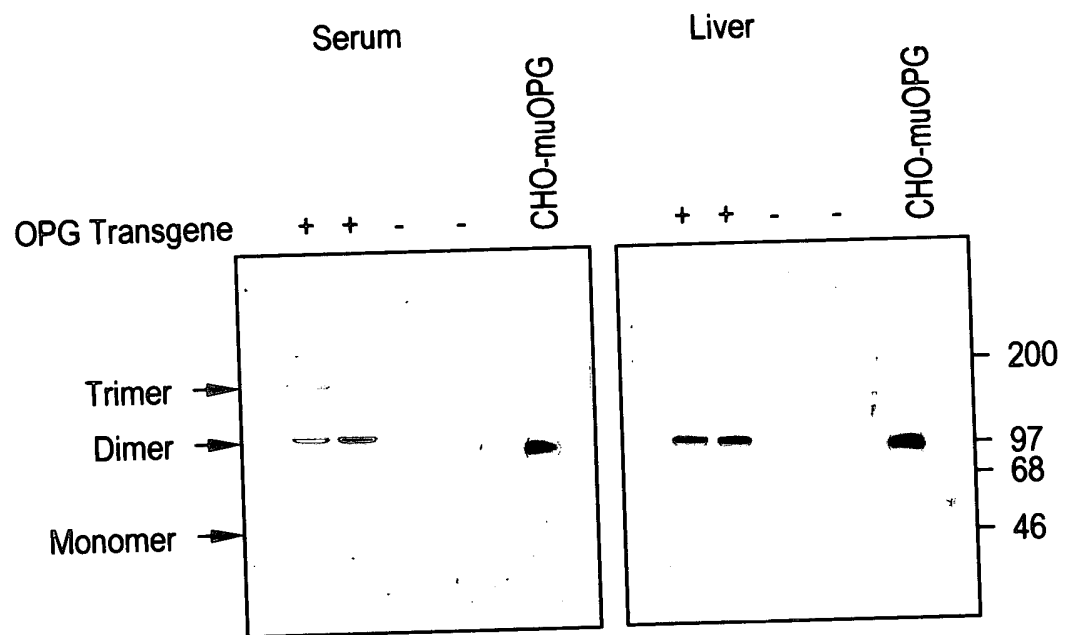


FIG. 19B

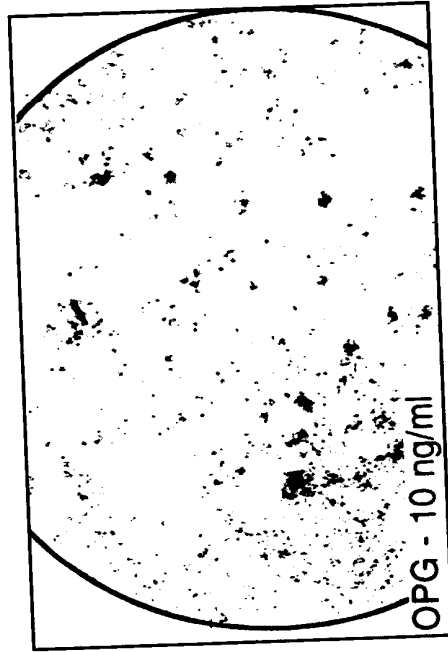


FIG. 19D



FIG. 19A

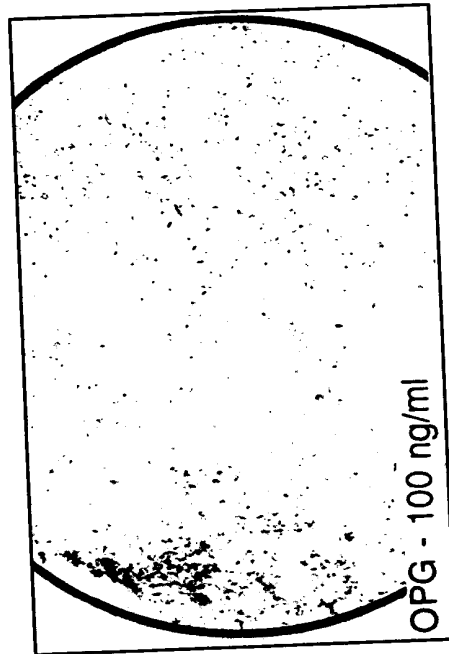


FIG. 19C

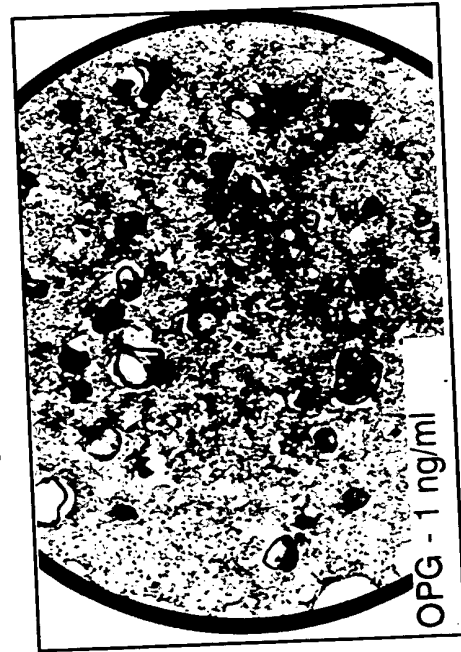


FIG. 19F

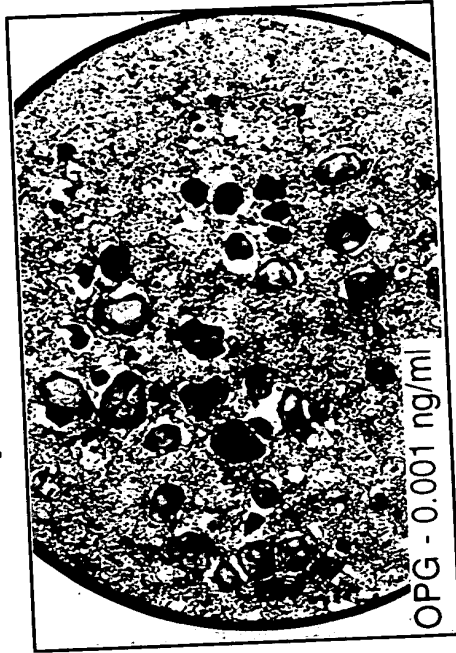


FIG. 19E

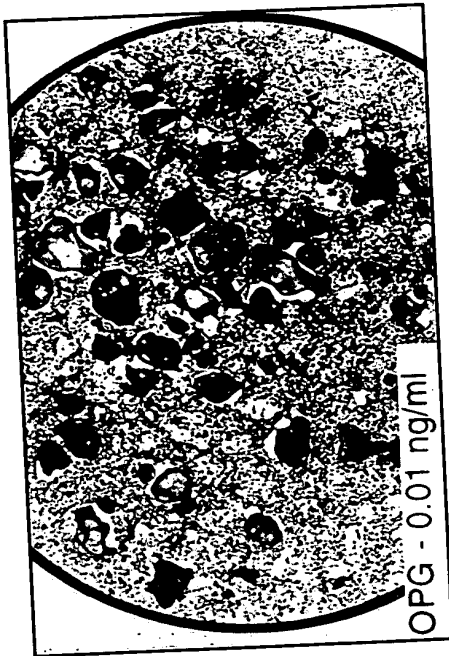


FIG. 19G

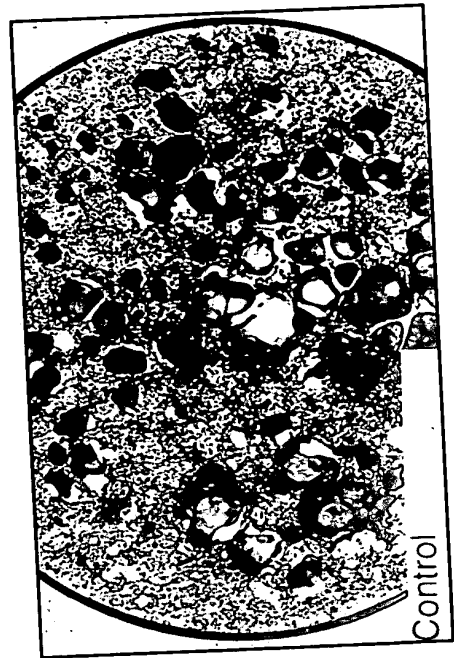


FIG.20

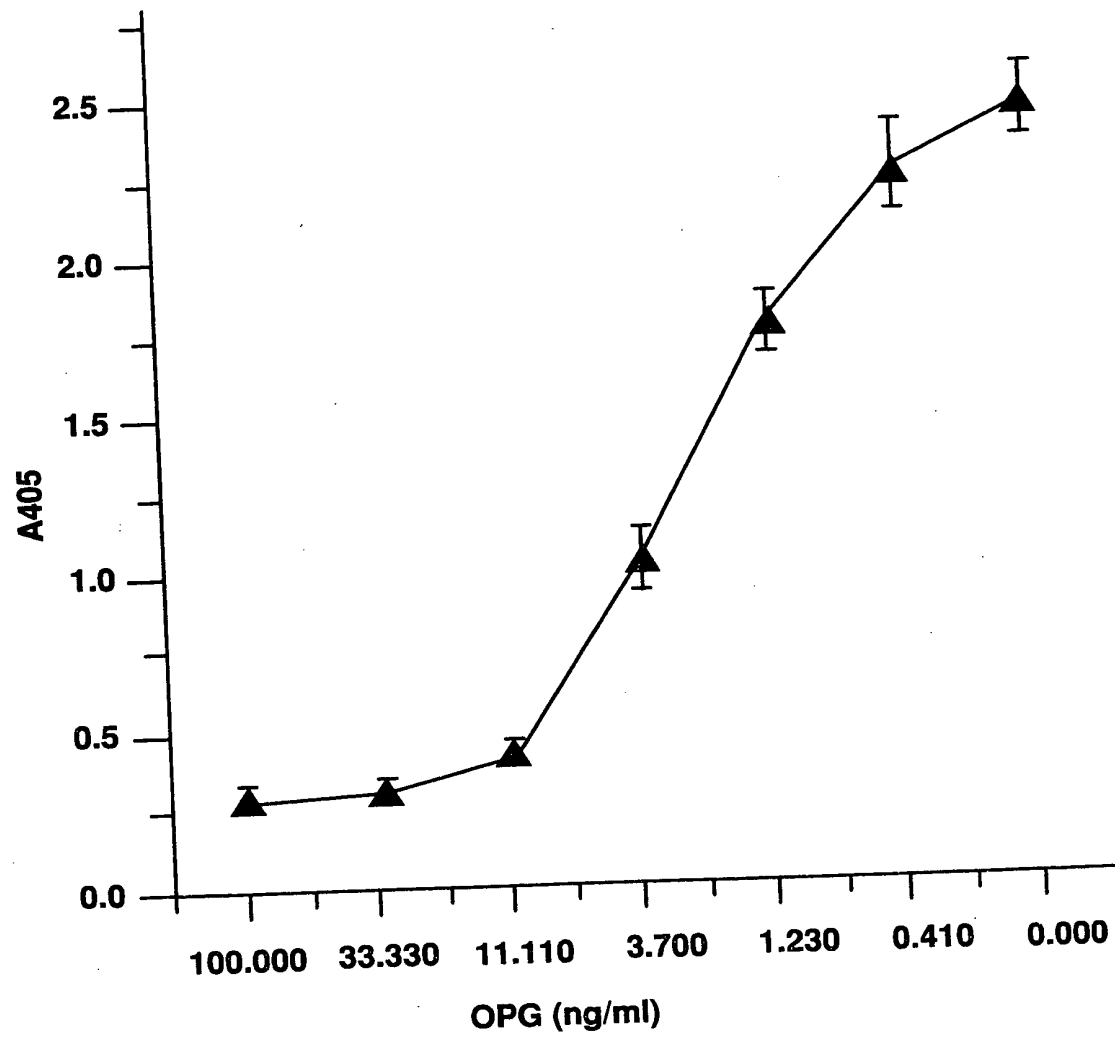
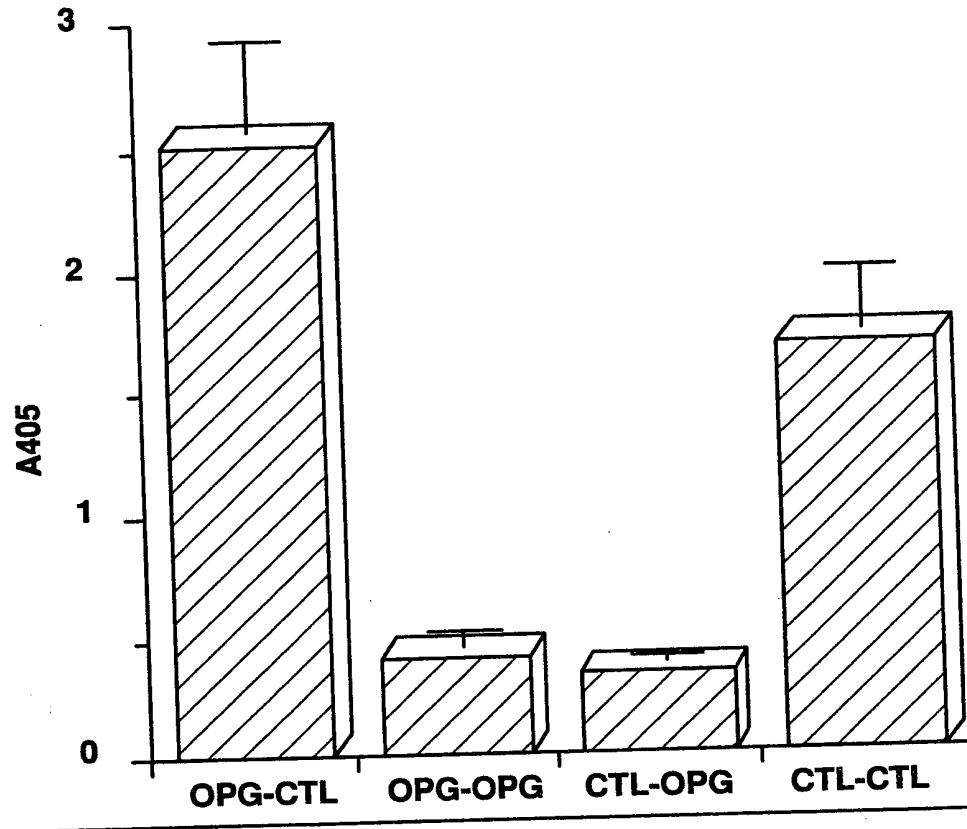


FIG.21



Legend

Growth
Bone marrow
cells
CSF -1

Intermediate
PGE2 + CSF-1

Terminal
ST2 cells
1,25 (OH)2 D3
Dexamethasone

4 days

2 days

8 - 10 days

Groups

CTL - CTL
 OPG - CTL
 OPG - OPG
 OPG - OPG

OPG

 100 ng/ml

 100 ng/ml

OPG

 100 ng/ml
 100 ng/ml

FIG. 22A

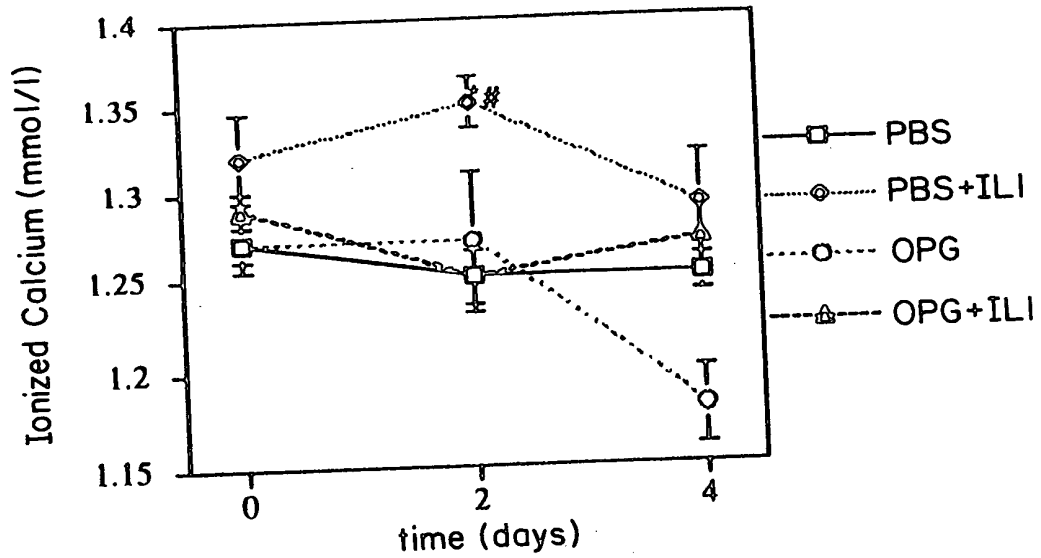
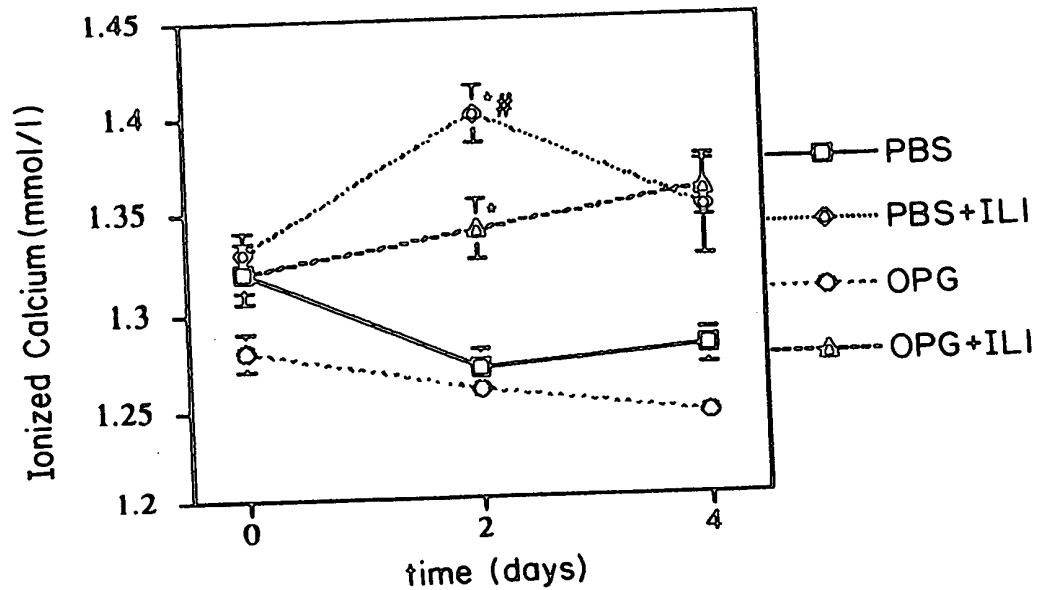


FIG. 22B



* Different to PBS, $p < 0.05$

Different to OPG + IL1, $p < 0.05$

FIG. 23A

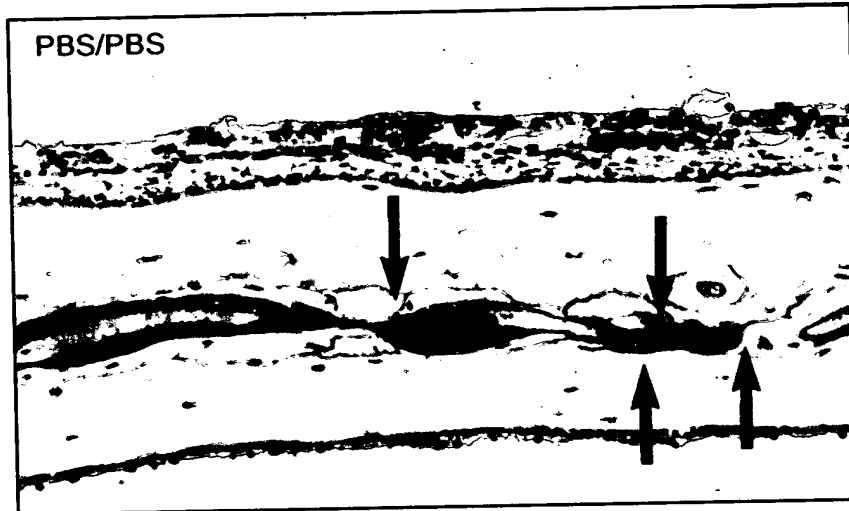


FIG. 23B

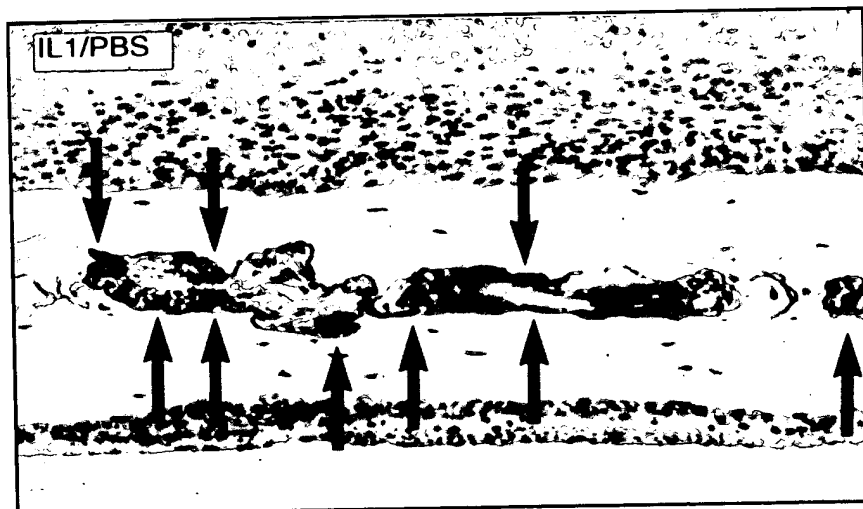


FIG. 23C

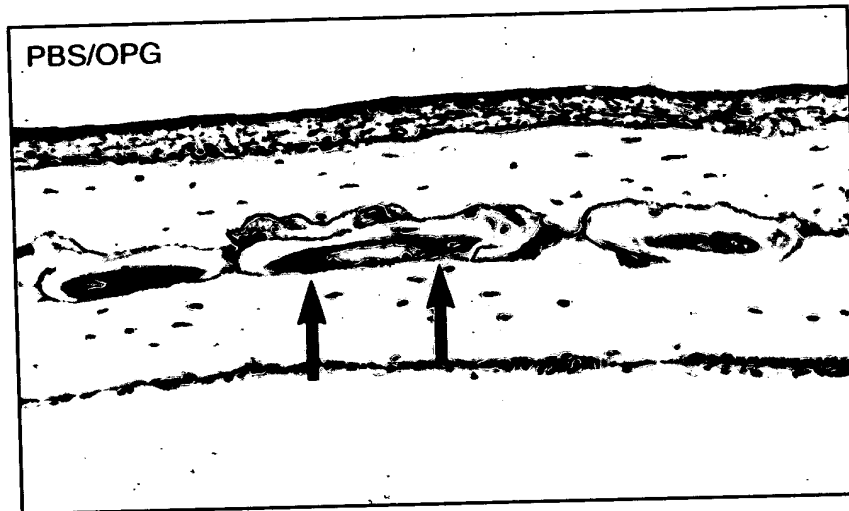


FIG. 23D

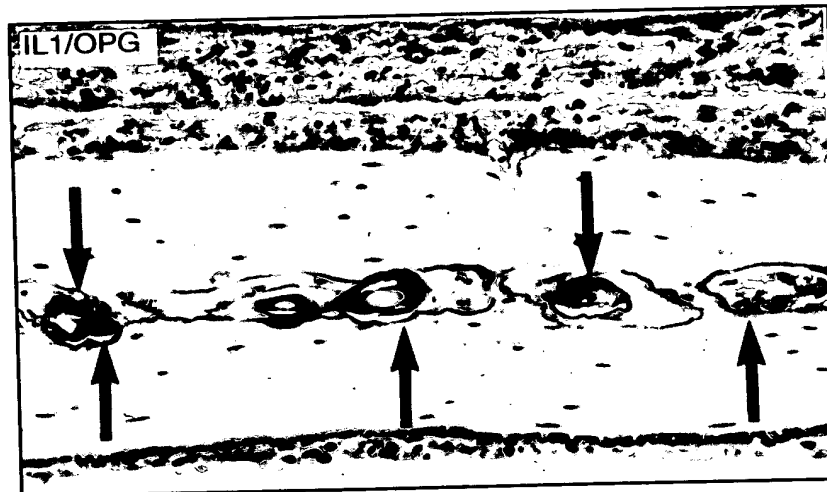


FIG. 24B

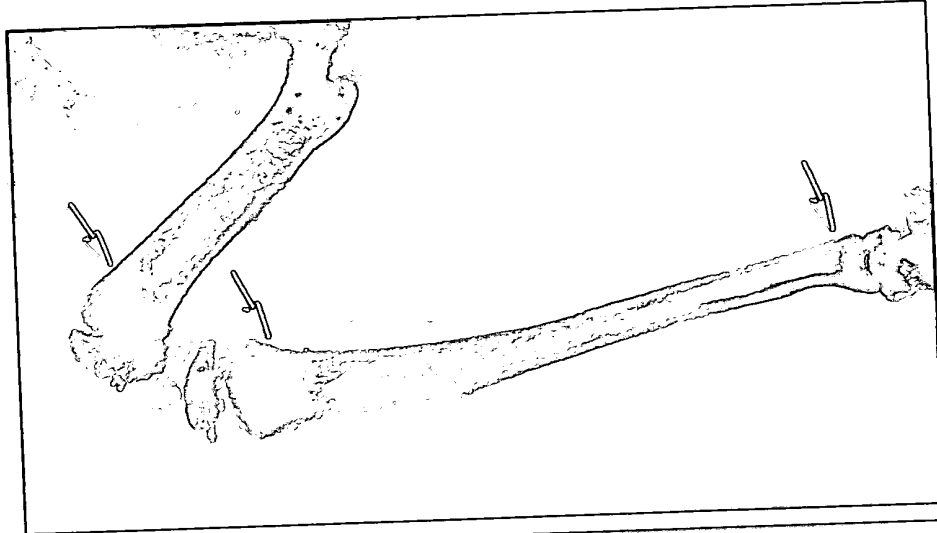


FIG. 24A

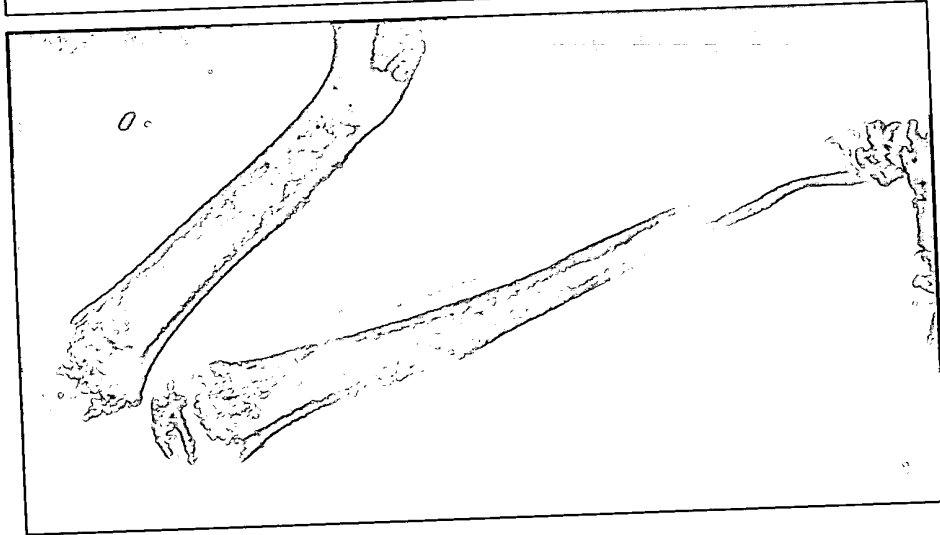
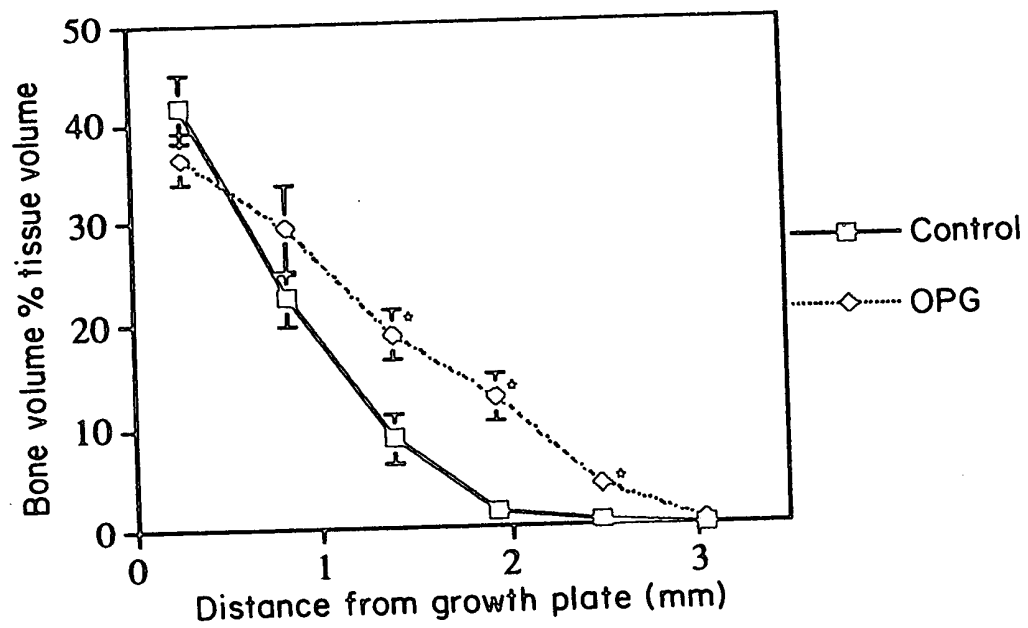


FIG. 25



* Different to control $p < 0.01$

FIG. 26A



FIG. 26B



FIG. 27

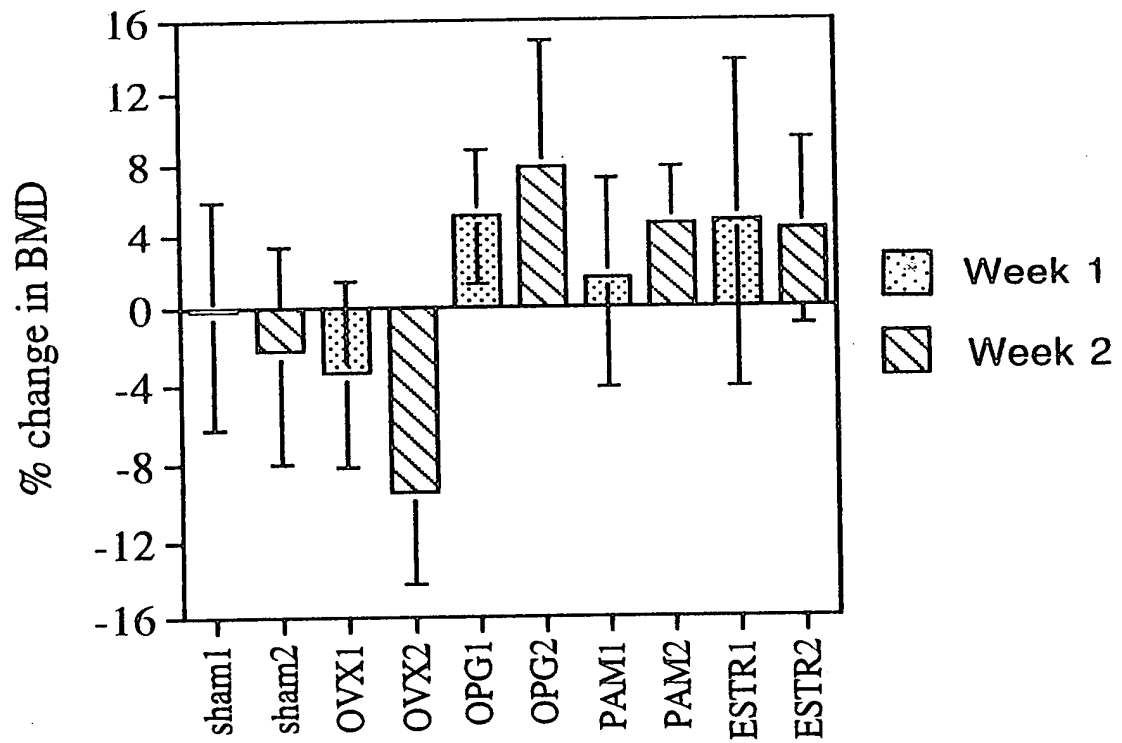
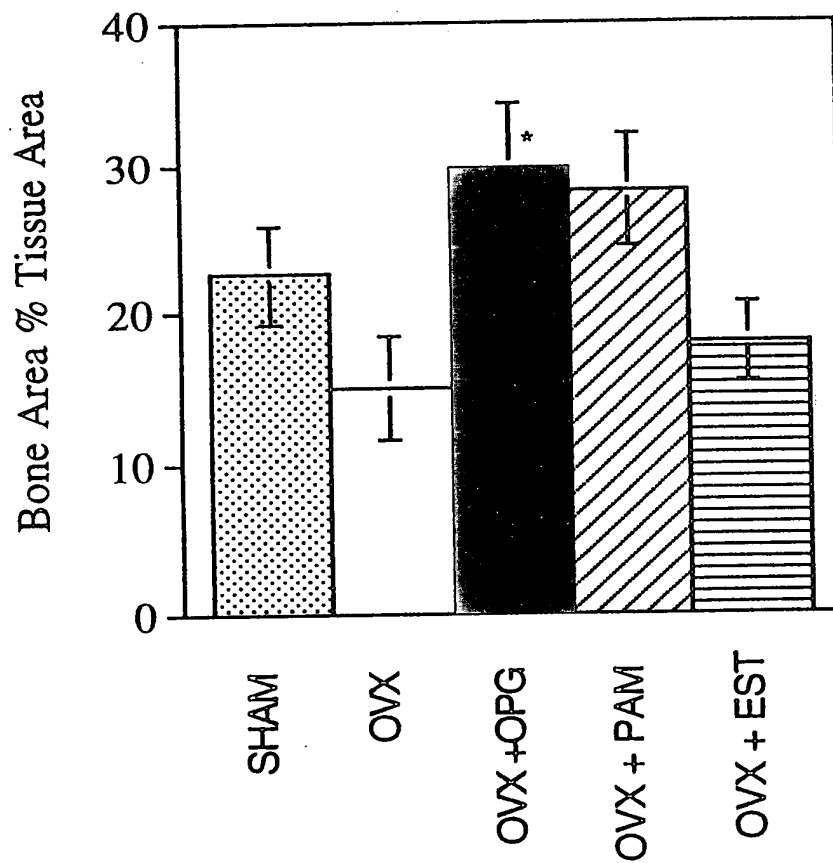


FIG. 28



* Different to OVX $p < 0.05$

FIG. 29A

DraIII

1
CATGGGAAATGTCAGAGTGGAGAACCACACCGAGTGCCACTGCAGCACTTGTTATTATCA
-----+-----+-----+-----+-----+-----+ 60
GTACCCCTTTACAGTCTCACCTCTTGGTGTGGCTCACGGTGACGTCGTGAACAATAATAGT

61
CAAATCCTAATAGTTTGCAGTGGGCCTTGCTGATGATGGCTGACTTGCTCAAAAGGAAAA
-----+-----+-----+-----+-----+-----+ 120
GTTTAGGATTATCAAACGTCACCCGGAACGACTACTACCGACTGAACGAGTTTTCCTTTT

121
TTAATTTGTCCAGTGTCTATGGCTTTGTGAGATAAAACCCTCCTTTTCCTTGCCATACCA
-----+-----+-----+-----+-----+-----+ 180
AATTAAACAGGTACAGATACCGAAACACTCTATTTTGGGAGGAAAAGGAACGGTATGGT

181
TTTTTAACCTGCTTTGAGAATATACTGCAGCTTTATTGCTTTTCTCCTTATCCTACAATA
-----+-----+-----+-----+-----+-----+ 240
AAAAATTGGACGAAACTCTTATATGACGTCGAAATAACGAAAAGAGGAATAGGATGTTAT

241
TAATCAGTAGTCTTGATCTTTTCATTTGGAATGAAATATGGCATTAGCATGACCATAAA
-----+-----+-----+-----+-----+-----+ 300
ATTAGTCATCAGAACTAGAAAAGTAAACCTTACTTTATACCGTAAATCGTACTGGTATTT

301
AAGCTGATTCCACTGGAAATAAAGTCTTTTAAATCATCACTCTATCACTGAATTCTAATT
-----+-----+-----+-----+-----+-----+ 360
TTCGACTAAGGTGACCTTTATTTAGAAAATTTAGTAGTGAGATAGTGAAGTAAAGATTAA

361
TTTTCTGAAAAGTTTCAAGCCAGTTACTTTTGATAGGATTAACGGAAGGGAGTGAGCCAG
-----+-----+-----+-----+-----+-----+ 420
AAAAGACTTTTCAAAGTTCGGTCAATGAAAACATCCTAATTGCCTTCCCTCACTCGGTC

XcmI

421
TGGGTGAGGTGGGTTCCTCATGTAGTCAATGGCCTAATACTGGAGAATCTTATTCTAACCA
-----+-----+-----+-----+-----+-----+ 480
ACCCACTCCACCAAGGGTACATCAGTTACCGGATTATGACCTCTTAGAATAAGATTGGT

481
AGCCTTCCAGAGCAAGCTGTGAGCCCCTCAGACAGTGGGCTACTCATGAGACAGTCCATT
-----+-----+-----+-----+-----+-----+ 540
TCGGAAGGTCTCGTTCGACACTCGGGGAGTCTGTCAACCGATGAGTACTCTGTCAGGTAA

541
GGGGTAAAGGAAGAAAATATAACTTCTATTTCTATTTCATTGTCACATTGTCTTTAGATGC
-----+-----+-----+-----+-----+-----+ 600
CCCCATTTCTTCTTTTATATTGAAGATAAAGATAAGTAAACGTGTAACAGAAATCTACG

601
CCATTTGGGTGAGTTTATAGAAGTACAGCTACATTAAAAAATAGAACTGATAATAGATA
-----+-----+-----+-----+-----+-----+ 660
GGTAAACCCACTCAAATATCTTCATGTGATGTAATTTTTTATCTTGACTATTATCTAT

FIG. 29B

AGGCTTTAAAAAACTTCATTCATCACCAGTTTGTCAAGATTCCATTTCAAAGTGAAAAA
661 -----+-----+-----+-----+-----+-----+-----+ 720
TCCGAAATTTTTTTGAAGTAAGTAGTGGTCAAACAGTTCTAAGGTAAAGTTTCACTTTTT
CCAATTTCTAACGGGTGGTAAACACAGCAGATGGCAGGGTGAAAAATTAAAGTGAGTGC
721 -----+-----+-----+-----+-----+-----+-----+ 780
GGTTAAAGATTGCCCAACCATTGTGTGCTCTACCGTCCCACTTTTAAATTTCACTCACG
ATGTACCTTTAAAGAAACACTGAAATGCACACACATTACTTAACCTGCTCATTCATTTAT
781 -----+-----+-----+-----+-----+-----+-----+ 840
TACATGGAAATTTCTTGTGACTTTACGTGTGTGTAATGAATTGGACGAGTAAGTAAATA
TTACATATAGTCTTGGGTGTACAAAATTTAGAAATAAATACATATGGGGGCGGGGCCTTA
841 -----+-----+-----+-----+-----+-----+-----+ 900
AATGTATATCAGAACCACATGTTTTAAATCTTTATTTATGTATACCCCCGCCCCGGAAT
GCTGCACAAATAGGATGCGCGGCGGGCCTTGGTAGGGGCGGAGCCTTAGCTGCACAAATA
901 -----+-----+-----+-----+-----+-----+-----+ 960
CGACGTGTTTATCCTACGCGCCGCCGGAACCATCCCCGCTCGGAATCGACGTGTTTAT
GGATGCGCGGCGGGCCTTGGTGGGGGCGGGGCCTAAGCTGCGCAAGTGGTACACAGCTCA
961 -----+-----+-----+-----+-----+-----+-----+ 1020
CCTACGCGCCGCCGGAACCACCCCCGCCCGGATTGACGCGTTACCATGTGTGCGAGT
GGGCTGCGATTTGCGGCCAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTA
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
CCCCGCGCTAAAGCGCGGTTTGAAGTGCCGTTAGGATCGCACTTCGACCATCCTAAAT
TCCCCGCTGCCATCATGGTTCGACCATTGAACTGCATCGTCGCCGTGTCCCAAATATGG
1081 -----+-----+-----+-----+-----+-----+-----+ 1140
AGGGGCGACGGTAGTACCAAGCTGGTAAGTTGACGTAGCAGCGGCACAGGGTTTTATACC
GGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCC
1141 -----+-----+-----+-----+-----+-----+-----+ 1200
CCTAACCGTTCTTGCCTCTGGATGGGACCGGAGGCGAGTCCTTGCTCAAGTTCATGAAGG
AAAGAATGACCACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGA
1201 -----+-----+-----+-----+-----+-----+-----+ 1260
TTTCTTACTGGTGTGGAGAAGTCACCTTCCATTTGTCTTAGACCACTAATACCATCCT
AAACCTGGTTCTCCATTCTTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTTC
1261 -----+-----+-----+-----+-----+-----+-----+ 1320
TTTGGACCAAGAGGTAAGGACTCTTCTTAGCTGGAAATTTCTGTCTTAATTATATCAAG
SacI BstXI
| |
TCAGTAGAGAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGCCAAAAGTTTGGATG
1321 -----+-----+-----+-----+-----+-----+-----+ 1380
AGTCATCTCTTGAGTTTCTTGGTGGTGCTCCTCGAGTAAAGAACGGTTTTCAAACCTAC

FIG. 29D

BspLU11I
|
AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAA
2041 -----+-----+-----+-----+-----+-----+ 2100
TCCCCTATTGCGTCCTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATT

AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAA
2101 -----+-----+-----+-----+-----+-----+ 2160
TTTCCGGCGCAACGACCGCAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTT

TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC
2161 -----+-----+-----+-----+-----+-----+ 2220
AGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCTGATATTTCTATGGTCCGCAAAGG

CCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTC
2221 -----+-----+-----+-----+-----+-----+ 2280
GGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAG

CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAG
2281 -----+-----+-----+-----+-----+-----+ 2340
GCGGAAAGAGGGGAAGCCCTTCGCACCGCGAAAGAGTATCGAGTGCGACATCCATAGAGTC

TTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGA
2341 -----+-----+-----+-----+-----+-----+ 2400
AAGCCACATCCAGCAAGCGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCT

CCGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC
2401 -----+-----+-----+-----+-----+-----+ 2460
GGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAG

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTAC
2461 -----+-----+-----+-----+-----+-----+ 2520
CGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATG

AGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTG
2521 -----+-----+-----+-----+-----+-----+ 2580
TCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCCTGTCATAAACCATAGAC

CGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGTAGCTCTTGATCCGGCAAACA
2581 -----+-----+-----+-----+-----+-----+ 2640
GCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGT

HgiEII
|
AACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAA
2641 -----+-----+-----+-----+-----+-----+ 2700
TTGGTGGCGACCATCGCCACCAAAAAACAAACGTTTCGTCGTCTAATGCGCGTCTTTTTT

AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGAACGAAAA
2701 -----+-----+-----+-----+-----+-----+ 2760
TCCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTT

FIG. 29E

CTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT
2761 -----+-----+-----+-----+-----+-----+ 2820
GAGTGCAATTCCTAAAACCAGTACTCTAATAGTTTTTCCTAGAAGTGGATCTAGGAAAA

AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAG
2821 -----+-----+-----+-----+-----+-----+ 2880
TTTAATTTTTTACTTCAAATTTAGTTAGATTTTCATATATACTCATTGAACCAGACTGTC

TTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCAT
2881 -----+-----+-----+-----+-----+-----+ 2940
AATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTA

AGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCC
2941 -----+-----+-----+-----+-----+-----+ 3000
TCAACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGG

CAGTGCTGCAATGATACCGCGAGACCCACGCTCACGGGCTCCAGATTTATCAGCAATAAA
3001 -----+-----+-----+-----+-----+-----+ 3060
GTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTT

CCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCA
3061 -----+-----+-----+-----+-----+-----+ 3120
GGTCGGTCGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGT

GTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAA
3121 -----+-----+-----+-----+-----+-----+ 3180
CAGATAATTAACAACGGCCCTTCGATCTCATTCATCAAGCGGTCAATTATCAAACGCGTT

CGTTGTTGCCATTGCTGCAGGCATCGTGGTGTACGCTCGTCGTTTGGTATGGCTTCATT
3181 -----+-----+-----+-----+-----+-----+ 3240
GCAACAACGGTAACGACGTCCGTAGCACCACAGTGCGAGCAGCAAACCATACCGAAGTAA

CAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGC
3241 -----+-----+-----+-----+-----+-----+ 3300
GTGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCG

PvuI EaeI
| GdiII
GGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCGAGTGTTATCACT
3301 -----+-----+-----+-----+-----+-----+ 3360
CCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGA

CATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTC
3361 -----+-----+-----+-----+-----+-----+ 3420
GTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAG

BcgI
|
TGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTG
3421 -----+-----+-----+-----+-----+-----+ 3480
ACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAAC

FIG. 29F

CTCTTGCCCGGCGTCAACACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCT
3481 -----+-----+-----+-----+-----+ 3540
GAGAACGGGCGCAGTTGTGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTCACGA
CATCATTTGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATC
3541 -----+-----+-----+-----+-----+ 3600
GTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAACTCTAG
CAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAG
3601 -----+-----+-----+-----+-----+ 3660
GTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTC
CGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGAC
3661 -----+-----+-----+-----+-----+ 3720
GCAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATCCCGCTG
SspI
|
ACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATGAAGCATTTATCAGGG
3721 -----+-----+-----+-----+-----+ 3780
TGCCTTTACAACCTTATGAGTATGAGAAGGAAAAGTTATAATAACTTCGTAAATAGTCCC
TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGT
3781 -----+-----+-----+-----+-----+ 3840
AATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCA
TCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGAC
3841 -----+-----+-----+-----+-----+ 3900
AGGCGCGTGTAAGGGGCTTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTG
ATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAAGAATTCCCTGTGGA
3901 -----+-----+-----+-----+-----+ 3960
TAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTTCTTAAGGGACACCT
ATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAA
3961 -----+-----+-----+-----+-----+ 4020
TACACACAGTCAATCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTT
GCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCA
4021 -----+-----+-----+-----+-----+ 4080
CGTACGTAGAGTTAATCAGTCGTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGT
GAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCCTAACTCCGC
4081 -----+-----+-----+-----+-----+ 4140
CTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCG
CCATCCCGCCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTT
4141 -----+-----+-----+-----+-----+ 4200
GGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAA

FIG. 29G

SfiI
|
TTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAG
4201 -----+-----+-----+-----+-----+-----+ 4260
AAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTC

AvrII
|
GAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTGGTCGAGGCTCGCATCTCTCCTT
4261 -----+-----+-----+-----+-----+-----+ 4320
CTCCGAAAAAACCTCCGGATCCGAAAACGTTTTTCGACCAGCTCCGAGCGTAGAGAGGAA

CACGCGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGC
4321 -----+-----+-----+-----+-----+-----+ 4380
GTGCGCGGGCGGCGGGATGGACTCCGGCGGTAGGTGCGGCCAACTCAGCGCAAGACGGCG

CTCCCGCCTGTGGTGCCTCCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGT
4381 -----+-----+-----+-----+-----+-----+ 4440
GAGGGCGGACACCACGGAGGACTTGACGCAGGCGGCAGATCCATTCAAATTCGAGTCCA

NgoAIV
|
CGAGACCGGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCA
4441 -----+-----+-----+-----+-----+-----+ 4500
GCTCTGGCCCGGAAACAGGCCGCGAGGGAACCTCGGATGGATCTGAGTCGGCCGAGAGGT

CGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCC
4501 -----+-----+-----+-----+-----+-----+ 4560
GCGAAACGGACTGGGACGAACGAGTTGAGATGCAGAAACAAAGCAAAAGACAAGACGCGG

HpaI
|
GTTACAGATCCGTCGAGGAACTGAAAAACCAGAAAGTTAACTGGTAAGTTTAGTCTTTTT
4561 -----+-----+-----+-----+-----+-----+ 4620
CAATGTCTAGGCAGCTCCTTGACTTTTTTGGTCTTTCAATTGACCATTCAAATCAGAAAAA

Psp5II BamHI
| |
GTCTTTTATTTTCAAGTCCCGGATCCGGTGGTGGTGCAAATCAAAGAACTGCTCCTCAGTG
4621 -----+-----+-----+-----+-----+-----+ 4680
CAGAAAATAAAGTCCAGGGCCTAGGCCACCACCGTTTAGTTTCTTGACGAGGAGTCAC

GATGTTGCCTTTACTTCTAGGCCTGTACGGAAGTGTTACTTCTGCTCTAAAAGCTGCTGC
4681 -----+-----+-----+-----+-----+-----+ 4740
CTACAACGGAAATGAAGATCCGGACATGCCTTCACAATGAAGACGAGATTTTCGACGACG

HindIII XbaI
| |
AACAAGCTTCTAGACCACCATGAACAAGTTGCTGTGCTGCGCGCTCGTGTCTTCTGGACAT
4741 -----+-----+-----+-----+-----+-----+ 4800
TTGTTTCAAGATCTGGTGGTACTTGTTCACGACACGACGCGGAGCACAAAGACCTGTA

BssHII
|
TTGTTTCAAGATCTGGTGGTACTTGTTCACGACACGACGCGGAGCACAAAGACCTGTA

b M N K L L C C A L V F L D I -

FIG. 29H

CTCCATTAAGTGGACCACCCAGGAAACGTTTCCTCCAAAGTACCTTCATTATGACGAAGA
4801 -----+-----+-----+-----+-----+ 4860
GAGGTAATTCACCTGGTGGGTCCTTTGCAAAGGAGGTTTCATGGAAGTAATACTGCTTCT
b S I K W T T Q E T F P P K Y L H Y D E E -

KpnI
|
AACCTCTCATCAGCTGTTGTGTGACAAATGTCCTCCTGGTACCTACCTAAAACAACACTG
4861 -----+-----+-----+-----+-----+ 4920
TTGGAGAGTAGTCGACAACACACTGTTTACAGGAGGACCATGGATGGATTTTGTGTGAC
b T S H Q L L C D K C P P G T Y L K Q H C -

TACAGCAAAGTGGAAAGACCGTGTGCGCCCTTGCCCTGACCACTACTACACAGACAGCTG
4921 -----+-----+-----+-----+-----+ 4980
ATGTCGTTTCACCTTCTGGCACACGCGGGGAACGGGACTGGTGATGATGTGTCTGTCTGAC
b T A K W K T V C A P C P D H Y Y T D S W -

GCACACCAGTGACGAGTGTCTATACTGCAGCCCCGTGTGCAAGGAGCTGCAGTACGTCAA
4981 -----+-----+-----+-----+-----+ 5040
CGTGTGGTCACTGCTCACAGATATGACGTCGGGGCACACGTTTCCTCGACGTCATGCAGTT
b H T S D E C L Y C S P V C K E L Q Y V K -

RleAI BsmI
| |
GCAGGAGTGCAATCGCACCCACAACCGCGTGTGCGAATGCAAGGAAGGGCGCTACCTTGA
5041 -----+-----+-----+-----+-----+ 5100
CGTCCTCACGTTAGCGTGGGTGTTGGCGCACACGCTTACGTTCCCTTCCCGCGATGGAAGT
b Q E C N R T H N R V C E C K E G R Y L E -

GATAGAGTTCTGCTTGAAACATAGGAGCTGCCCTCCTGGATTTGGAGTGGTGCAAGCTGG
5101 -----+-----+-----+-----+-----+ 5160
CTATCTCAAGACGAACTTTGTATCCTCGACGGGAGGACCTAAACCTCACCACGTTGAC
b I E F C L K H R S C P P G F G V V Q A G -

BsmBI
|
AACCCCAGAGCGAAATACAGTTTGCAAAGATGTCCAGATGGGTCTTCTCAAATGAGAC
5161 -----+-----+-----+-----+-----+ 5220
TTGGGGTCTCGCTTTATGTCAAACGTTTCTACAGGTCTACCCAAGAAGAGTTTACTCTG
b T P E R N T V C K R C P D G F F S N E T -

GTCATCTAAAGCACCTGTAGAAAACACACAAATTGCAGTGTCTTTGGTCTCCTGCTAAC
5221 -----+-----+-----+-----+-----+ 5280
CAGTAGATTTCTGTTGGACATCTTTTGTGTGTTTAAACGTACAGAAACCAGAGGACGATTG
b S S K A P C R K H T N C S V F G L L L T -

BspEI
|
TCAGAAAGGAAATGCAACACACGACAACATATGTTCCGGAAACAGTGAATCAACTCAAAA
5281 -----+-----+-----+-----+-----+ 5340
AGTCTTTCCTTTACGTTGTGTGCTGTTGTATACAAGGCCTTTGTCACTTAGTTGAGTTTT
b Q K G N A T H D N I C S G N S E S T Q K -

FIG. 29 I

SalI BmgI
| |
AGTCGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTC
5341 -----+-----+-----+-----+-----+ 5400
TCAGCTGTTTTGAGTGTGTACGGGTGGCACGGGTCTGGACTTGAGGACCCCCCTGGCAG
b V D K T H T C P P C P A P E L L G G P S -

AGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCCTGAGGT
5401 -----+-----+-----+-----+-----+ 5460
TCAGAAGGAGAAGGGGGGTTTTGGGTTCTGTGGGAGTACTAGAGGGCCTGGGGACTCCA
b V F L F P P K P K D T L M I S R T P E V -

BtrI
|
CACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGT
5461 -----+-----+-----+-----+-----+ 5520
GTGTACGCACCACCACCTGCACTCGGTGCTTCTGGGACTCCAGTTCAAGTTGACCATGCA
b T C V V V D V S H E D P E V K F N W Y V -

SacII
|
GGACGGCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCAC
5521 -----+-----+-----+-----+-----+ 5580
CCTGCCGCACCTCCACGTATTACGGTTCTGTTTCGGCGCCCTCCTCGTCATGTTGTCGTG
b D G V E V H N A K T K P R E E Q Y N S T -

GTACCGTGTGGTCAGCGTCTCACCCTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTA
5581 -----+-----+-----+-----+-----+ 5640
CATGGCACACCAGTCGCAGGAGTGGCAGGACGTGGTCTGACCGACTTACCGTTCCCTCAT
b Y R V V S V L T V L H Q D W L N G K E Y -

CAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCATCGAGAAAACCATCTCCAAGC
5641 -----+-----+-----+-----+-----+ 5700
GTTACGTTCCAGAGGTTGTTTCGGGAGGGTCGGGGGTAGCTCTTTTGGTAGAGGTTTCG
b K C K V S N K A L P A P I E K T I S K A -

SmaI
|
CAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAGCTGAC
5701 -----+-----+-----+-----+-----+ 5760
GTTTCCCGTCGGGGCTCTTGGTGTCCACATGTGGGACGGGGGTAGGGCCCTACTCGACTG
b K G Q P R E P Q V Y T L P P S R D E L T -

CAAGAACCAGGTGACCTGACCTGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGT
5761 -----+-----+-----+-----+-----+ 5820
GTTCTTGGTCCAGTCGGACTGGACGGACCAGTTTCCGAAGATAGGGTCGCTGTAGCGGCA
b K N Q V S L T C L V K G F Y P S D I A V -

GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGGA
5821 -----+-----+-----+-----+-----+ 5880
CCTCACCTCTCGTTACCCGTCGGCCTCTTGTGATGTTCTGGTGCGGAGGGCACGACCT
b E W E S N G Q P E N N Y K T T P P V L D -

FIG. 29J

AarI
|

CTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCA
5881 -----+-----+-----+-----+-----+ 5940
GAGGCTGCCGAGGAAGAAGGAGATGTCGTTTCGAGTGGCACCTGTTCTCGTCCACCGTCGT
b S D G S F F L Y S K L T V D K S R W Q Q -

SapI
|

GGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAA
5941 -----+-----+-----+-----+-----+ 6000
CCCCTTGCAGAAGAGTACGAGGCACTACGTACTCCGAGACGTGTTGGTGATGTGCGTCTT
b G N V F S C S V M H E A L H N H Y T Q K -

GAGCCTCTCCCTGTCTCCGGGTAAATGATAACTCGAC
6001 -----+-----+-----+-----+ 6037
CTCGGAGAGGGACAGAGGCCCATTTACTATTGAGCTG
b S L S L S P G K * *

FIG. 30A-1

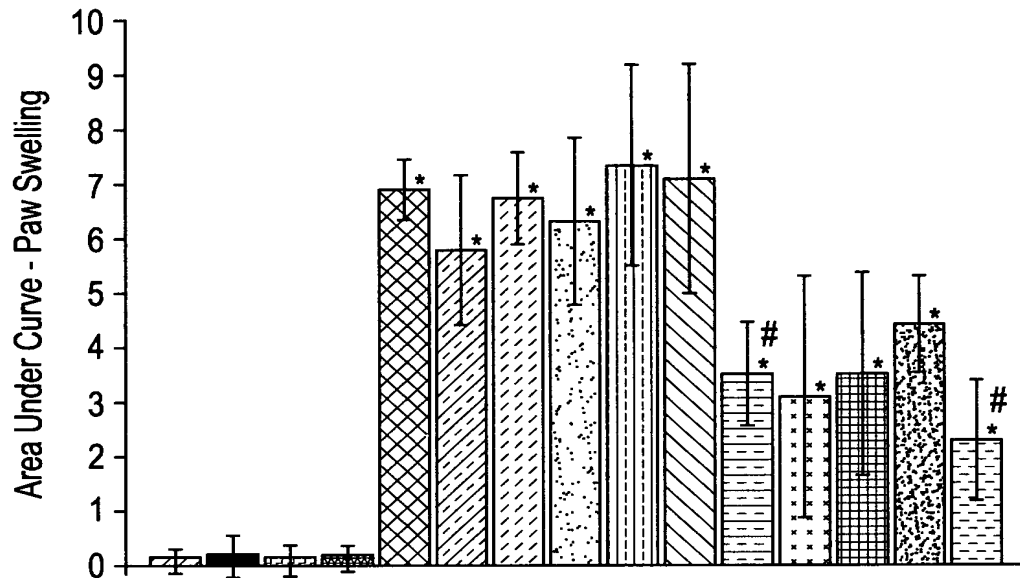
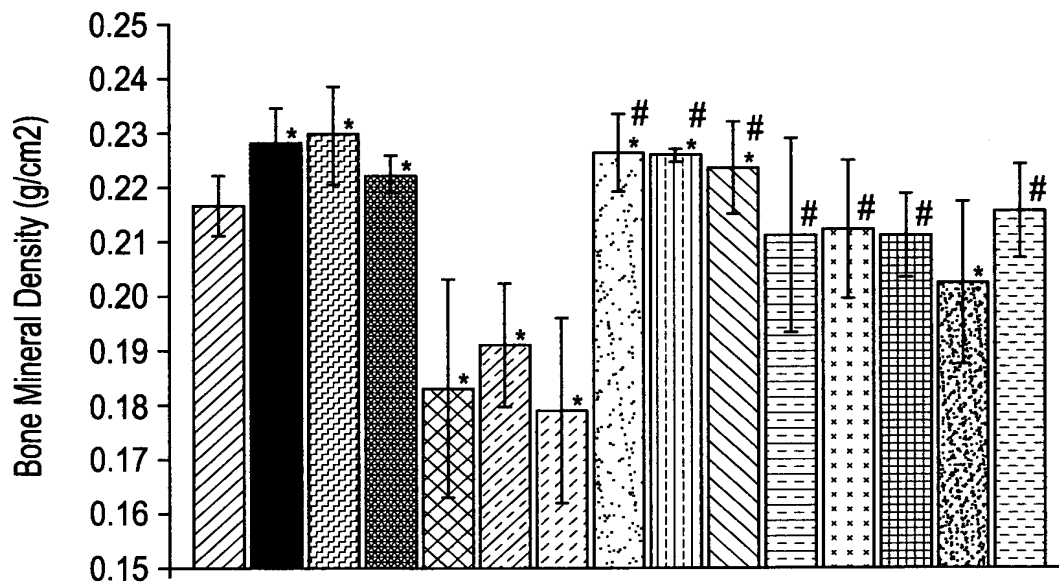


FIG. 30A-2



- | | |
|-----------------------------------|---------------------------------------|
| Normal (NT) | AdA + 1.0 mg/kg OPG-Fc (s.c.) |
| Normal + 4 mg/kg OPG-Fc (s.c.) | AdA + 0.25 mg/kg OPG-Fc (s.c.) |
| Normal + 1.0 mg/kg OPG-Fc (s.c.) | 15.0 mg/kg/hr IL-1ra (2ML1) |
| Normal + 0.25 mg/kg OPG-Fc (s.c.) | 5.0 mg/kg/hr IL-1ra (2ML1) |
| AdA Control | 1.0 mg/kg/hr IL-1ra (2ML1) |
| AdA + CSEP (2ML1) | 0.2 mg/kg/hr IL-1ra (2ML1) |
| AdA + OPG Placebo (s.c.) | AdA + 0.07 mg/kg Dexamethasone (s.c.) |
| AdA + 4 mg/kg OPG-Fc (s.c.) | |

FIG. 30B-1

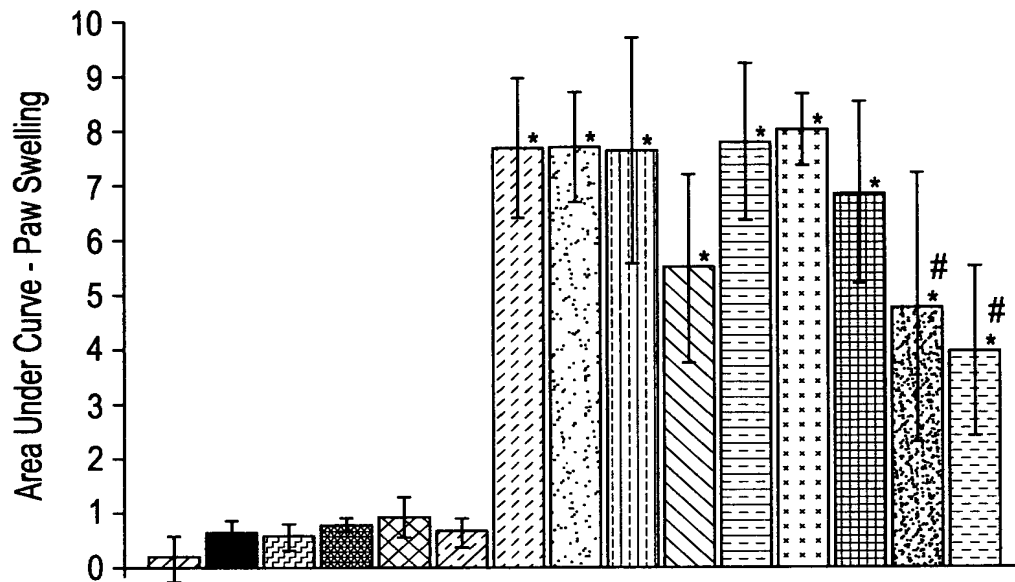
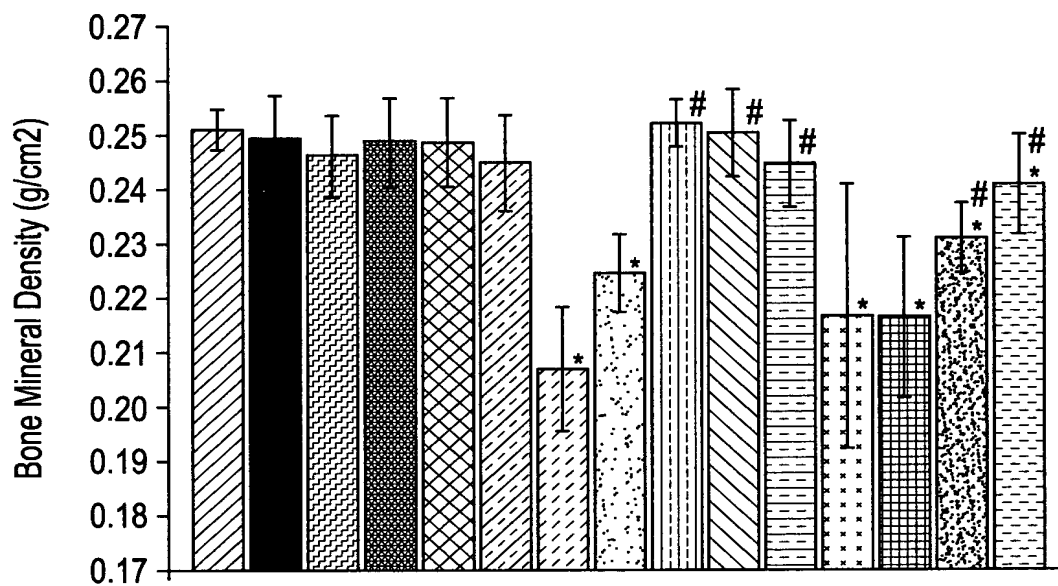


FIG. 30B-2



- | | |
|-------------------------------------|---------------------------------------|
| Normal | AdA + 1.0 mg/kg OPG-Fc (s.c.) |
| Normal + 1.0 mg/kg OPG-Fc (s.c.) | AdA + 0.25 mg/kg OPG-Fc (s.c.) |
| Normal + 0.25 mg/kg OPG-Fc (s.c.) | AdA + 0.0625 mg/kg OPG-Fc (s.c.) |
| Normal + 0.0625 mg/kg OPG-Fc (s.c.) | AdA + 0.016 mg/kg OPG-Fc (s.c.) |
| Normal + 0.016 mg/kg OPG-Fc (s.c.) | AdA + 0.004 mg/kg OPG-Fc (s.c.) |
| Normal + 0.004 mg/kg OPG-Fc (s.c.) | AdA + 5.0 mg/kg/hr IL-1ra (2ML1) |
| AdA control | AdA + 0.07 mg/kg Dexamethasone (s.c.) |
| AdA + OPG Placebo (s.c.) | |

FIG. 31A

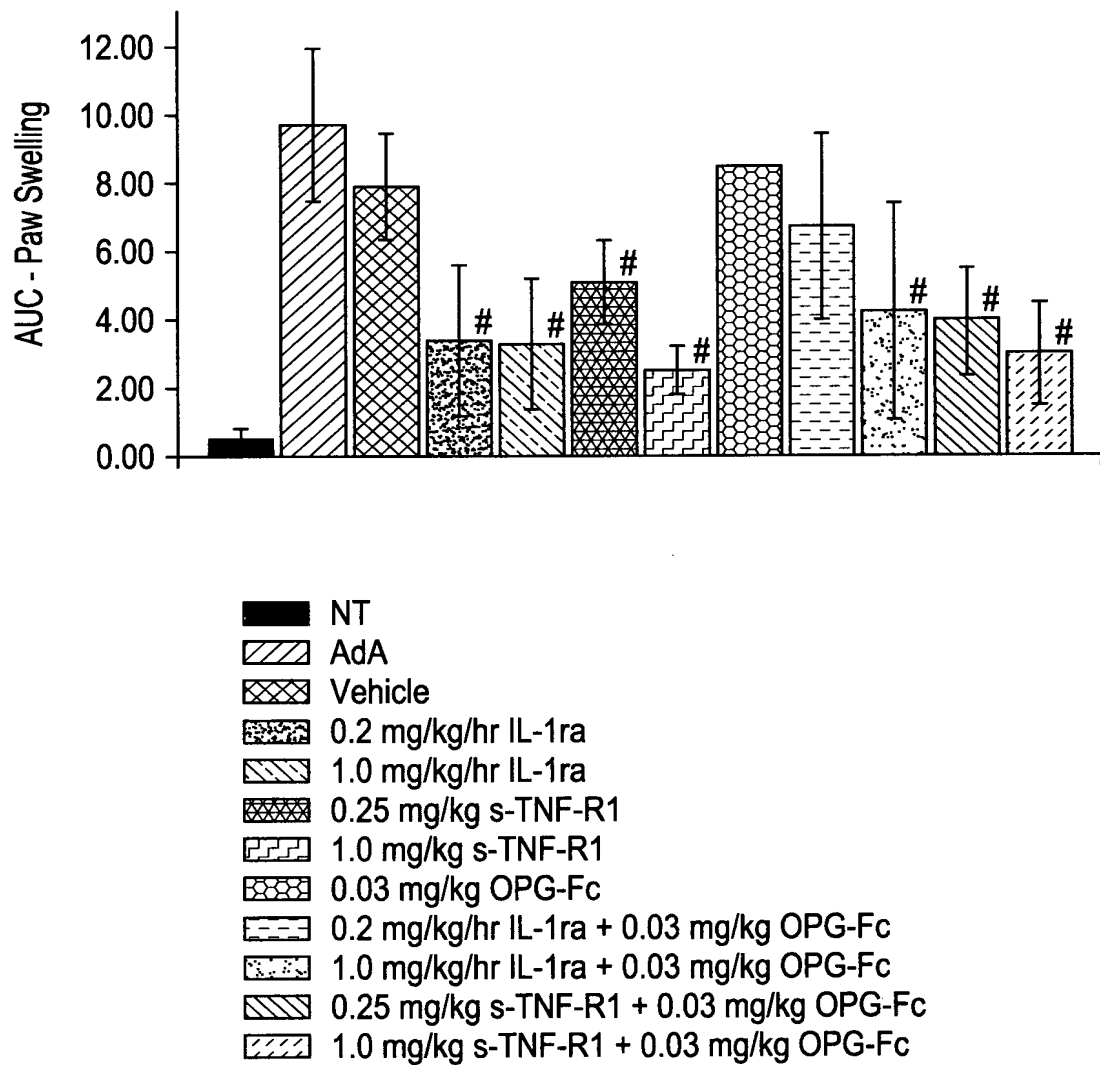


FIG. 31B

